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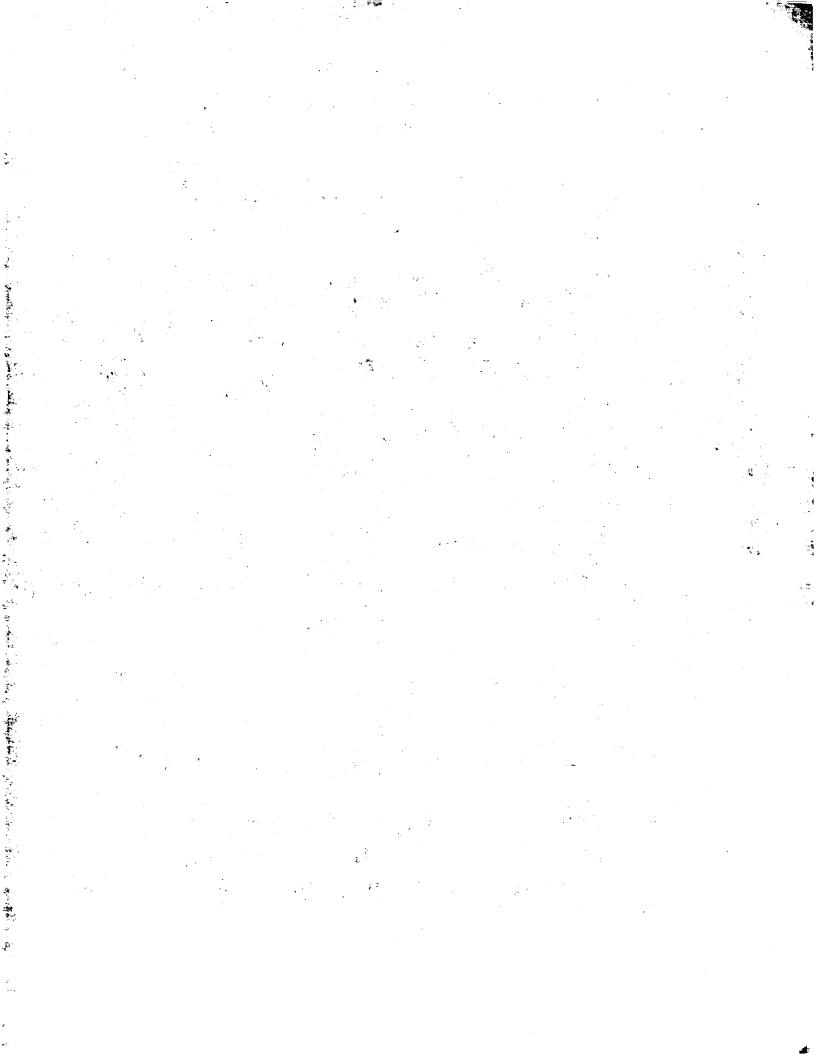
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STIC-Biotech/ChemLib

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From: Sent: To: Subject:

Rao, Manjunath N.

Wednesday, April 18, 2001 3:50 PM

STIC-Biotech/ChemLib

Sequence search request for 09/262,126

From: Manjunath N. Rao

Art Unit 1652, Room 10D04

Phone: 306-5681

Date: 4-18-01

Please search the following as soon as possible for application with serial number 09/262,126

SEQ ID NO:. 1 against all nucleic acid databases including issued patents database and pending application database and provide a print of all results.

SEQ ID NO: 2-4 against all protein databases including issued patents database and pending application database. and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao Art Unit 1652 Room CM1, 10D04 Phone 306-5681

Edward Hart Technical Info Specialist STIC / Biotech CM1 12C14 Tel: 305-9203

MANJUNATH N. RAO

Patent Examiner AU 1652, CM1 10D04 703-306-5681

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Access DB# 40481

SEARCH REQUEST FORM

Scientific and Technical Information Center

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Requester's Full Name:	•	Examiner # :	
Art Unit:	Phone Number 30	Serial Number:	
Mail Rox and Blag/Room	Location:	Results Format Preferred (circ	cie): PAPER DISK E-MAI
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Inventors (please provide full	names):	· · · · · · · · · · · · · · · · · · ·	
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Searches run against the Nucleic Acid Pending database will produce two sets of results, with the extensions .rnpm

Searches run against the Amino Acid Pending database will produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

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Pullulanase, micro-organisms producing the preparation thereof as well as its use patent; EP 0605040-A 8 06-JUL-1994;

SOLVAY (BE)
Other publication JP 6217770 940809
Other publication CN 1990325 940803
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Other publication AU 527593 940707
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Sequence 9
AR000475
AR000475.1
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Deweer, P. and Amory, A.
Expression system for novel pullulanase
Patent: US 5736375-A 9 07-APR-1998;
Location/Qualifiers
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1909	601 ggagatetteetgaaggaaactaecaatataaagtggetttaaatgatagetggaataat
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Patent: US 5817498-A 8 06-OCT-1998;
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540	caagatgtaaccgctgttttggcaggtaccttccaacatatttttggaggttccgattgg	481	D Q
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1729	CATGACGACAGCAAATAAGGATATTCCAGTGACATCTGTGAAGGATGCAAGTCTTGGT	1670	B

3889	GACAAATGGGGAAATATCATTGTTGTTATAAACCCCAAATAAAACTGTAGCAACCATCAAT	3830	/ Db
2640	acaaatggggaaatatcattgttgtttataacccaaataaaactgtagcaaccatcaa	2581	Qy
3829	CAATTCCTAAATAGTCCAGAGAACACAGTGGCCTATGAATTAACTGATCATGTTAATAAA	3770	Db
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3769	CTTCGTCTTGATCACCCAGCCTTCCGCATGACGACAGCTAATGAAATCAATAGCCACCTC	3710	Db
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3709	GATTGGAGCAGGAAAGCTCAATATCCAGATGTTTTCAACTATTATAGCGGGCTAATCCAC	3650	Db
2460	attggagcaggaaagctcaatatccagatgttttcaactattatagcgggctaatcca	2401	Оу
3649	CTTCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAGGCGATGCGGTCAATGAGTTT	3590	DЬ
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3589	GCACAAGCAGTTGTTATGACCTCACAAGGCGTTCCATTCATGCAAGGCGGGGAAGAAATG	3530	Дb
2340	cacaagoagttgttatgacctcacaaggogttccattcatgcaaggogggaagaaat		Qy
3529	AAAATAGCCCTAAGCAATCCTAATGATTCCGAAGCGGATCGGATTAAAATGGATGAACTC	3470	da
2280	aaatagccctaagcaatcctaatgattccgaagcggatcggattaaaatggatgaact	N	Оу
3469	TCTTCACCAGGTGAGACAATTAACTATGTCACAAGTCATGATAACTACACCCTTTGGGAC	3410	Дb
2220	cttcaccaggtgagacaattaactatgtcacaagtcatgataactacaccctttggga	_	Qy
3409	GCAACAGGCTTAACTGATGCAATTAAGAATGGCGTTGAGGGGAGTATTAATGACTTTACC		фd
2160	caacaggcttaactgatgcaattaagaatggcgttgaggggggtattaatgactttac	2101	Qy
3349	TTACGAAACGCGTTGGACGGCAATGTCTTTGATTCTTCCGCTCAAGGTTTTGCGACAGGT	3290	фd
2100	tacqaaacqcqttqqacqqcaatqtctttqattcttccqctcaaqqttttqcqacaqq	2041	Qy
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3229	ATCCAGGAATTGCACTTTACGGTGAGCCATGGACGGGTGGAACCTCTGCACTGCCAGAT	3170	Дb
1980	atccaggaattgcactttacggtgagccatggacgggtggaacctctgcactgccaga	1921	γŷ
3169	TRANTGGCGCTGCTTGGAAAAGACACGATGTCCAAAGCTGCCTCGGAGCTTCATGCTATT	3110	Db
1920	taatggcgctgcttggaaaagacacgatgtccaaagctgcctcggagcttcatgctat	œ	Qy
3109	ATTATTGATTCCCTTAAGTATTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGAC	3050	Db
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3049	CCAACGGATCAGGTACTGGAAATGAAATTGCANGCNGAAAGGCCAATGGTTCAAAAATTT	2990	Дb
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2869	ACAAATGCGAATGCTCATTAAAAGAGTTTAAGGAAATGGTTCTTTCACTCCAT	2810	Db
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1 (bases 1 to 4464)

Deweer, P. and Amory, A.

Process for the production of novel

Process 5721128-A 8 24-FEB-1998;

Location/Qualifiers
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Deweer,P. and Amory,A.
Process for the production
Patent: US 5721128-A 9 24-F
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1680	gtgaacacattggggttaacatggatgttgtctataatcatacctttgccacgcaaat	1621	Qy
2869	ACAAATGCGAATGGTAATGCTCGTATAAAAGAGTTTAAGGAAATGGTTCTTTCACTCCAT	2810	Дb
1620	caaatgcgaatggtaatgctcgtataaaagagtttaaggaaatggttctttcactcca	1561	Qy
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2749	TTACTCATGTTCAGCTTATGCCTGTTTTCGCATCTAACAGTGTCGATGAAACTGATCC		DЬ
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2569	CATATTACGCCAAAGAATATAGAAGATGAGGTCATCTATGAAATGGATGTCCGTGA		뭥
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2269	CAGAAAGCAACCTTTAAAAGTCTGGGCACCCAACTTCTACTCAAGTAAATGTTCTT	N	Db
1020	acacagaaagcaacaacctttaaagtctgggcaccaacttctactcaagtaaatgttctt	961	Qy
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Matches 2793; Conservative
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                          GGAGATCTTCCTGAAGGAAACTACCAATATAAAGTGGCTTTAAATGATAGCTGGAATAAT
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                                                                  GCACCTGATAATCACAGTACTTTATTAAAAAAAGGTGACTAACAATCTCTATCAATTCTCA
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DeWeer, P. and Amory, A.
Process for the saccharification of
Patent: US 5731174 A 8 24-MAR-1998;
Location/Qualifiers
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1680 2929	cgtgaacacattggggttaacatggatgttgtctataatcatactttgccacgcaaatc	1621 2870	dg dy
96	CAAATGCGAATGCTCGTATAAAAAAGAGTTTAACGAAATGCTTCTTCACTCCAT	œ	рь
1620	ctccat	1561	Qy
2809	ACCCAAGATAATTGGGGTTATGACCCTCGCAACTATGATGTTCCTGAAGGGCAGTATGCT		Db
1560	cccaagataattggggttatgaccctcgcaactatgatgttcctgaagggcagtatgc	1501	γo
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1440		1381	Qy
2629	TTTTCCATTGACCCTAATTCGGGTATGAAAAATAAAGGGAAGTATTTGGCTCTTACAGAA	2570	라
1380	tttccattgaccctaattcgggtatgaaaataaagggaagtatttggctcttacag	1321	Qγ
2569	AAACATATTACGCCAAAGAATATAGAAGATGAGGTCATCTATGAAATGGATGTCCGTGAC	2510	밁
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2509	GGAACGAGAGGCATGATTGTGGACCTGGCTAAAACAGATCCTGCTGGCTG	2450	Db
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1200	aggccaaggctctacccgaacggctgttgatccttatgcaactgcgattgcaccaaa	1141	Qy
2389	GTGTGTGGGAAGCACGGTTAATCAAAACCTTGAAAATTGGTATTACATGTATGAGGTA	2330	, Db
1140	gtgtgtgggaagcaacggttaatcaaaaccttgaaaattggtattacatgtatgaggta	1081	Qy
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2269	ACACAGAAAGCAACCATTAAAGTCTGGGCACCAACTTCTACTCAAGTAAATGTTCTT	2210	ర్జ
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2209	CGTAATGTGCTTAATTCATCACACTACTACTATTCAGGAGATGATCTTGGGAATACCTAT	2150	Дb
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780	tttcgtatattccgtccactcatgcagtctatgacacaattaataatcctaatgcggat	721	Qy
1969	CCGAGTTACCCATCTGACAACATTAATTTAACAGTCCCTGCCGGCGGTGCACACGTCACT	1910	рь

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1860 3109	1801 attattgattcccttaagtattgggtcaatgagtatcatattgacggcttccgttttgac 	
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2029	1970 TTTTCGTATATTCCGTCCACTCATGCAGTCTATGACACAATTAATAATCCTAATGCGGAT	

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A38130 2784 bp DNA Sequence 10 from Patent EP0605040. A38130 A38130.1 GI:2294741

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Deweer, P. and Amory, A.

Pullulanase, micro-organisms producing the preparation thereof as well as its use patent; EP 0605040-A 10 06-JUL-1994;

SOLVAN (BE)

Other publication JP 6217770 940809
Other publication CA 2112028 940829
Other publication CN 1090325 940803
Other publication CN 1090325 940803
Other publication BE 1007523 951010
Other publication BE 1007723 950516
Other publication BE 1007733 950516
Other publication BE 100783 940913.
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2700 2700	LLGCCGAGCGGGAAATGGGCAATCAATGCTACGAGCGGTAAGGTAGGAGAATCCACCCTT	2641 2641
2640 2640	gacaaatggggaaatatcattgttgtttataacccaaataaaactgtagcaaccatcaat 	2581 2581
2580 2580	CABILCCLABALAGICCAGAGAACACAGIGGCCTAIGAALLAACLGALCALGILLAALAAA	2521 2521
2520 2520	cttcgtcttgatcacccagccttccgcatgacgacagctbatgaaatcaatagccacctc	2461 2461
2460 2460	galtggagcaggaaagctcaatatccagatgttttcaactattatagcgggctaatccac 	2401 2401
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2340 2340	gcacaagcagttgttatgacctcacaaggcgttccattcatgcaaggcgggggaagaaatg	2281 2281
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2220 2220	tottcaccaggtgagacaattaactatgtcacaagtcatgataactacaccctttgggac	2161 2161
2160 2160	gcaacaggottaactgatgcaattaagaatggcgttgaggggagtattaatgactttacc	2101 2101
2100 2100	ttacyanacycyttyyacyycaatytctttyattcttccyctcaayyttttycyacasyt	2041
2040	gatcagcttctgacaaaaggagctcaaaaaaggcatgggagtagcggtgtttaatgacaat	1981 1981
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ALIGNMENTS

RESULT

x87941 standard; DNA;

2794 BP.

Bacillus deramificans mature pullulanase coding sequence.

22-NOV-1999 X87941;

(first entry)

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Miller BS, Shetty JK;
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                                                                                                                                                     Pullulanase; enzyme engineering; starch; saccharification; straight chain amylase; alpha-dextrin 6-glucano-hydrolase; alpha-1,6-glucosidase; ss.
                    (GEMV ) GENENCOR INT INC
                                  04-MAR-1998;
                                                 03-MAR-1999;
                                                                                                                                        Bacillus deramificans.
                                                                10-SEP-1999
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                                  9805-0034630
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                                                                                             /EC_number= "3.2.1.41"
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Best Local Similarity 100.0%;
Matches 2793; Conservative
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15-JUL-1993;
19-NOV-1993;
                                                                                                                                              This sequence codes for the mature pullulanase enzyme isolated from Bacillus deramificans 7 89.117D. The pullulanase hydrolyses the alpha-1.6-glycosidic bonds of amylopectin and of pullulan. The enzyme can be used (with glucoamylase) for saccharification of starch. Typical applications include use as anti-staling additives in bread making and brewing, in preparation of low calorie foods and to clarify fruit juices.
                                                                                                                                                                                                                                New pullulanase from Bacillus deramificans - 1 saccharification etc., with good stability over ranges, also related DNA vectors, transformed
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The present sequence encodes a trimmed enzyme isolated from Bacillus sp. APC-9603. The present specification also describes: (1) a vector containing the DNA encoding a trimmed enzyme; (2) a recombinant microbe transformed by the DNA; and (3) preparation of a trimmed enzyme in which the microbe of (2) is cultured and the trimmed enzyme is collected from the culture. The method can prepare a trimmed enzyme of wide substrate specificity having heat resistance and being active in acid region efficiently.
                                                                                                                                                                                                                                           Claim
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Sequence 3934 BP; 1200 A; 756 C; 908 G; 1070 T; 0 other;

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Pullulanase; genetically

pulB; debranching e
engineered variant;

enzyme; sequence

amylopectin; potato; wheat

thermostable;

corn;

Pullulanase 05-MAY-2000

(pulB)

nucleotide entry) **289960**

standard;

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RESULT Z89960 ID Z8 XX XX AC Z8 XX DT O5 XX DT O5 XX Pt XX P
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Best Local Similarity 53.0%;
Matches 856; Conservative
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(IATR )
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P-PSDB; R23787.
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resistant pullanase can be produced in large amts. using a suitable
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                                                                                                                                                                                                                                                                                                                                                                                                                                  beta-galactosidase, beta-mannosidase, beta-mannanase, endoglucanase or pullulanase activity. Vectors and host cells are also claimed. A method is provided for producing the enzymes by recombinant techniques. A claimed method for generating glucose from soluble cell oligosaccharides comprises contacting a sample (selected from dairy products, fruit juice, detergent, textile, guar gum, animal feed, plant biomass or waste product) containing oligosaccharides (selected from maltose, cellobiose, lactose, sucrose, raffinose, stacchyose, verbascose, cellulose, starch, amylose, glycogen, disaccharides, polysaccharides and pullulan) with one of the claimed disaccharides and pullulan) with one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosidase enzymes from organisms of the genera Staphlothermus, Pyrococcus and Thermococcus - for deriving sugar from oligosaccharides, useful in the e.g. food processing, textile or
 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (6GP3) that grows optimally at 85 degC. The sequence shows 53% nucleic acid identity to an alpha destrom 6 glucanohydrolase of Caldocellum saccharolyticum. The invention provides 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 14a-e;
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P-PSDB; W49871.
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06-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caldocellum saccharolyticum. The invention provides 18 polynucleotides (see V36907-24) coding for thermostable glycosidases (see W49888-75) having glucosidase, alpha-galactosidase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This isolated polynucleotide comprises a coding region for pullulanase 6GP3 (see W49871) from a Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                       claimed glycosidases such that glucose is produced.
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                                           Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays pharmaceutical compositions and vaccines for Streptococcus
        Claim 1; Page 900-906; 1409pp; English
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Rosen CA;
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                                                                                                                                                                                                                                                                                                                                   pneumoniae genome fragment SEQ ID NO:132
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CC The present invention describes a computer readable medium which has CC the nucleotide sequences SEQ ID NO:1 to 391 (VS2134 to V52524) recorded CC on it, or a representative fragment or a sequence at least 95% identical CC SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae GEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a CC probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced CC from an organism, amplifying nucleic acid molecules whose nucleotide CC sequence is homologous to amplification primers derived from the sequences of the S. pneumoniae genome to prime the amplification and CC isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present CC invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
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Sequence 9541 BP; 2886 A; 2081 C; 1691 G; 2883 T; 0 other;

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0; Mismatches 518;
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                                                                                                                                                 1450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE
                                                                                                                                                                            1921
                                                                        DNA;
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Pred. No. 1
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le-11;
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Best Local S
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                                                                                                                                                                                                  can be recombinantly expressed using standard recombinant methodology. The GBS antigens of the invention can be used as vaccine components for the treatment or prophylaxis of diseases and symptoms mediated by Streptococcus infection, especially group A Streptococcus (S. pyogenes), GBS or S. agalactiae, S. dysgalactiae, S. uberis, S. nocardia, as well as Staphylococcus aureus. The vaccines are administered to those individuals at risk of GBS infection, particularly pregnant women and infants for sepsis, meningitis, and pneumonia, as well as immunocompromised individuals, such as those with diabetes, liver disease or cancer. The vaccines also have vetinary applications, such as for the treatment of mastitis in cattle. The present sequence represents a DNA encoding 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                               1508 ataattggggttatgaccctcgcaactatgatgttcctgaagggcagtatgctacaaatg 1567
                                                                                                                                                                 Sequence 5058 BP; 1744 A; B16
                                                                                                                                                                                                                                                                                                                                                                                  Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rioux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group
                                                                                                                                                                                                                                                                                                                                                                                                                    Novel group B Streptococcus antigens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9942588-A2
                                                                                                                                                                                          antigens
                                                                                                                                                                                                                                                                                                                                                         invention provides Group B Streptococcus
                                                                                                                                                                                                                                                                                                                                               nucleic acids (X91103-X91111) encoding
                       cgaatggt---aatgctcgtataaaagagtttaaggaaatggttctttcactccatcgtg 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-540309/45.
DB; Y27354, Y27355,
caaaagatccatcagcacgtatcgccgaattaaaaacaattaatacatgatattcataaac 4444
                                                acaattggggctatgacccacagagctattttgctctttctgggatgtattcagagaaac 4384
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                                                                                                               Similarity
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                                                                                                   Conservative
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1362..1742
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763..1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
l..666
                                                                                                                                                                                                                                                                                                                                                                                                          prophylaxis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag-
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                                                                                                                                                                                                                                                                                                                                                                                 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mastitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumonia;
                                                                                                               2.7%;
51.1%;
                                                                                                                                                                                          invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GBS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charlebois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigens encoding
                                                                                                 Score 74.4; DB 20
Pred. No. 4.8e-11;
0; Mismatches 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tigen; vaccine; Streptococcus infection;
immunocompromise; diabetes; liver disea
                                                                                                                                                                                                                                                                                                                                                                                                         therapy
                                                                                                                                                                   966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamel
                                                                                                                                                                                                                                                                                                                                                                                                         useful as vaccine of Streptococcus
                                                                                                                                                                   1531
                                                                                                                                                                                                                                                                                                                                           the antigens. The GBS antigens
                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                   208;
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                                                                                                                                                                                                                                                                                                                                                        (GBS) antigens (Y27336-370)
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                                                                                                                           Length
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                     The present invention describes a novel nucleic acid sequence which is obtainable from potato plants and carries at least a portion of an isoamylase-type debranching enzyme (DBE) gene. Constructs containing the nucleic acid sequence can be used to alter the starch properties of plants such as potato, sweet potato, maize, wheat, barley, oat, cassava, pea or rice. The starch can have increased branching and/or shorter chain length, reduced peak viscosity, higher setback viscosity or increased viscosity onset temperature. By using an antisense sequence with greater homology to the native gene, greater inhibition can be achieved. The present sequence represents a pullanase type partial length potato DBE cDNA clone from the present invention.
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                                                                                                                                                                                           Example 2; Fig 10; 72pp; English.
                                                                                                                                                                                                                                                                 WPI; 1999-229220/19
                                                                                                                                                                                                                                                                                             Jobling SA,
                                                                                                                                                                                                                                                                                                                                                    06-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pullanase type partial length potato DBE cDNA clone
                                                                                                                                                                                                                                                                                                                       (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING
                                                                                                                                                                                                                     isolated potato isoamylase-type debranching enzyme gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caggaattgcactttacggtgagccatgga
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Sequence 784 BP; 209 A; 161 C;

185 G;

229 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                   ataattgggggtataatcctggtctctggggagttccaaagggaagctacgctagtaatg
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Search completed: April 22, Job time: 2716 sec 2001, 06:56:18

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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
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Perfect score:
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           Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.
        2786.4
2786.4
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US-08-474-140-9
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIG
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,140
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhiem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-41
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                                                                                                                                                                                                                                                                                                      APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULA
TITLE OF INVENTION: PRODUCE
TITLE OF INVENTION: PULLULA
NUMBER OF SEQUENCES: 15
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TELECOMMUNICATION INFORMA:
TELEPHONE: (202) 429-00
TELEFAX: (202) 293-1850
TELEX: 650 383-565
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4604 base pair:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DI
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TELEPHONE: (202) 429-0625
TELEPAX: (202) 293-1850
TELEFAX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
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Best Local Similarity 100.0%;
Matches 2793; Conservative
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3 1-630-8 No. 5721128 No. 5721128 LINFORMATION: LICANT: DEWEER, PHILIPPE JICANT: AMORY, ANTOINE JE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH LE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS LE OF INVENTION: PULLULANASE AND THE USES THEREOF SEQUENCES: 15	gtaagcccagaccacggtaaaaagtaatagaaaa 2794 	ggtcaagcagagggaagtgtccaagtaccaggtatatctatgatgatccttcatcaagag 2760 	ttgccgagcgggaaatggcaatcaatgctacgagcggtaaggtaggagaatccaccctt 2700 	gacaaatggggaaatatcattgttgtttataacccaaataaaactgtagcaaccatcaat 2640 	caattcctaaatagtccagagaacacagtggcctatgaattaactgatcatgttaataaa 2580 	cttcgtcttgatcacccagccttccgcatgacgacagctaatgaaatcaatagccacctc 2520 	gattggagcaggaaagctcaatatccagatgttttcaactattatagcgggctaatccac 2460 	Cttcgtanaaaaggcggcaacgacaatagttataatgcaggcgatgcggtcaatgagttt 2400 	gcacaagcagttgttatgacctcacaaggcgttccattcatgcaaggcggggaagaaatg 2340 	aaaatagccctaagcaatcctaatgattccgaagcggatcggattaaaatggatgaactc 2280 	tetteaceaggtgagacaattaactatgteacaagteatgataactacaccetttgggac 2220 	gcaacaggcttaactgatgcaattaagaatggcgttgaggggagtattaatgactttacc 2160 	ttacgasacgcgttggacggcsatgtctttgattcttccgctcaaggttttgcgacaggt 2100 	gatcagcttctgacaaaaggagctcaaaaaggcatgggagtagcggtgtttaatgacaat 2040 	aatccaggaattgcactttacggtgagccatggacgggtggaacctctgcactgccagat 1980

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TELERAS: (202) 293-1850
TELERAS: (202) 293-1850
TELERAS: 650 383-5605
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
15-08-477-630-8
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Best Local Similarity 100.0%;
Matches 2793; Conservative (
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION UNUBER: US/08/477,630
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELECOMMUNICATION INFORMATION:
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STREET: 2000 K Street, N
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
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                        gacaaatggggaaatatcattgttgtttataacccaaataaaactgtagcaaccatcaat
                                                                                          CARTICCTAAATAGTCCAGAGAACACAGTGGCCTATGAATTAACTGATCATGTTAATAAA
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                                                                                                                                                                                                                                                                         Query Match 99.7%; S
Best Local Similarity 100.0%;
Matches 2793; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BR
STREET: 2000 K Street
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
                                                                                                                                                                                                                  1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, E.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 411
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                              181
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4464 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                               attatcgttcgcactcaagattggaccaaagatgtgagcgctgaccgctacatagattta 240
                                                                                       agcaaaggaaatgaggtgtggcttgtagaaggaaacagccaaatttttataatgaaaaa
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                                ATTATCGTTCGCACTCAAGATTGGACCAAAGATGTGAGCGCTGACCGCTACATAGATTTA
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GCAAAGGAATGAGGTGTGGCTTATAGAAGGAAACAGCCAAATTTTTTATATAATGAAAAA 154 GCTGAGGATGAGGCTAAACCCGCTGTAAGCAACGCTTATTTTAGAGTGCTTCAAACCAG FOCTGGTTAAACTTAGCAGCTAAACCCGCTTAAGCAACGCTTATTTAGATGCTTCAAACCAG FOCTGGTTAAACTTAGCCAGCCGTTAACTCCTTGGGGAAGGANAAAGGGTGCTTCAAACCAG FOCTGGTTAAACTTAGCCAGCCGTTAACTCTTGGGGAAGGANAAAGGGGCTTTACGGTT FOCTGGTTAAACTTAGGCAGCCGTTAACTCTTGGGGAAGGANAAAATCGGTTATTAGGTTTACGGTT FOCTGGTTAAACTTAGGCAGCCGTTAACTCTTGGGGAAGGANAAAACTGGGTTTACGGTT FOCTGGTTAAACTAAGGAAATTAAGGATATTAGAATTACAACAAATTTTTGGAAGGTTCTTGGTAATTACGGTT FOCTGATAATCAACAATATAAGGATACTTTAACAACAAATTTTTGGAAGGTTCTTGGTAATTACGGTT FOCTGATAATCAACAATATAAGGATACTTTAACAACAAATTTTTGGAAGGTTCTTGGTAATTCCAATTTTAGAACTCTTTTGGAAGTTCTCTTCTGTAAAACTCTTTTTGGAAGTTCTCTTCCAATTTAAAAATTAAAAAATTGGTTATATAAAAAATCTCTTTTGGAAGTTCTCTCTC	32	atattacgccaaagaatatagaagatgaggtcatctatgaaatggatgtccgtga 	Db Qy
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GCNAAGGANATGAGGTTGGGCTTGTAGAAGGANACAGCCANATTTTTATATATAAAAA 154 atgctgaggatgcagccgtctaaagcagcgttatttagatgcttcaaaccag 360	08	ttatgacagtgcaacgggttctgtaacaaaaatcgtacctatgacggcatcgggcca 	Db Oy
GCNAMGGANATGAGGTGTGGCTTGTAGAAGGANACAGCCANATTTTTATATATGANAA 154 atgctgaggatgcagctaaacccggctgtaagcaacgcttatttagatgcttcaaaccag 360 illililililililililililililililililili	26	.caganagcaacacctttaaagtctgggcaccaacttctactcaagtaaatgttct 	DB QY
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GCAAAGGAAATGAGGTGTGGCTTGTAGAAGGAAACAGCCAAATTTTTATATAATGAAAAA 154 atgctgaggatgcagctaaacccgctgtaagcaacgcttatttagatgcttcaaaccag 360	00	tgtgagccatactctgtccattcgaacagatggctatcaggcaaagcaggtgatacc 	Оy
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GCAAAGGAAATGAGGTGTGGCTTGTAGAAGGAAACAGCCAAATTTTTATATAATGAAAAA 154 atgctgaggatgcagctaaacccgctgtaagcaacgcttatttagatgcttcaaaccag 360	00	acctgataatcacagtactttattaaaaaaggtgactaacaatctctatcaattctc 	Qy Db
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2460 3709	gattggagcaggaaagctcaatatccagatgttttcaactattatagcgggctaatccac 	3650	Оy
3649	TTCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAGGCGATGCGGTCAATGAGTTT	59	Db
O OD	CACAAGCAGTTGTTATGACCTCACAAGGCGTTCCATTCATGCAAGGCGGGGAAGAAAT	3530	, Db
2340	gcacaagcagttgttatgacctcacaaggcgttccattcatgcaaggcgggaagaaatg	2281	Qy
3529	AAAATAGCCCTAAGCAATCCTAATGATTCCGAAGCGGATCGGATTAAAATGGATGAACTC	3470	Дb
2280	aaatayccctaaycaatcctaatgattccgaagcggatcggat	2221	Qy
46		41	Db -
2220	cttcaccaggtgagacaattaactatgtcacaagtcatgataactacaccctttgggac	2161	Qy
3409	GCAACAGGCTTAACTGATGCAATTAAGAATGGCGTTGAGGGGAGTATTAATGACTTTACC	3350	DЬ
2160	caacaggcttaactgatgcaattaagaatggcgttgagggggggtattaatgactttacc	2101	Оy
w	THACGAAACGCGTTGGACGCAATGTCTTTGATTCTTCCGCTCAAGGTTTTGCGACAGGT	29	qa
2100	tacgaaacgcgttggacggcaatgtctttgattcttccgctcaaggttttgcgacaggt	2041	VΩ
3289	GATCAGCTTCTGACAAAAGGAGCTCAAAAAGGCATGGGAGTAGCGGTGTTTAATGACAAT	3230	DЬ
2040	atcagcttctgacaaaaggagctcaaaaaggcatgggagtagcggtgtttaatgacaa	1981	Qy
3229	ATTCAGGAATTGCACTTTACGGTGAGCCATGGACGGGTGGAACCTCTGCACTGCCAGAT	3170	Db
1980	atccaggaattgcactttacggtgagccatggacgggtggaacctctgcactgccagat		Qy
3169	TTAATGGCGCTGCTTGGAAAAGACACGATGTCCAAAGCTGCCTCGGAGCTTCATGCTATT	3110	Db
1920	taatggcgctgcttggaaaagacacgatgtccaaagctgcctcggagcttcatgctat	Œ	Qy
3109	ATTATTGATTCCCTTAAGTATTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGAC	3050	Db
1860	ttattgattcccttaagtattgggtcaatgagtatcatattgacggcttccgttttga	1801	Qy
3049	CCAACGGATCAGGTACTGGAAATGGAAATTGCANGCNGAAAGGCCCAATGGTTCAAAAATTT	2990	Db
1800	caacggatcaggtactggaaatgaaattgcangcngaaaggccaatggttcaaaaatt	74	Qy
2989	TCTGACTTCGATAAAATTGTACCAGAATATTATTACCGTACGATGATGCAGGTAATTATA	2930	дb
1740	ctgacttcgataaaattgtaccagaatattattaccgtacgatgatccaggtaattat	6	Qy
2929	CGTGAACACATTGGGGTTAACATGGATGTTGTCTATAATCATACCTTTGCCACGCAAATC	œ	DЬ
1680	gtgaacacattggggttaacatggatgttgtctataatcatacctttgccacgcaaatc	1621	Qy
2869	ACAAATGCGAATGGTAATGCTCGTATAAAAGAGTTTAAGGAAATGGTTCTTTCACTCCAT	2810	DЬ
1620	caaatgcgaatggtaatgctcgtataaaagagtttaaggaaatggttctttcactcca	1561	Qy
2809	ACCCAAGATAATTGGGGTTATGACCCTCGCAACTATGATGTTCCTGAAGGGCAGTATGCT	2750	Db
1560	ccaagataattggggttatgaccctcgcaactatgatgttcctgaagggcagtatgc	1501	Оу
2749	ATTACTCATGTTCAGCTTATGCCTGTTTTCGCATCTAACAGTGTCGAATGAAACTGATCCA	2690	Db
1500	tactcatgitcagcitatgcctgitttcgcatctaacagigicgatgaaacigatcca	1441	Qy
2689	AAAGGAACAAAGGCCCTGACAACGTAAAGACGGGGATAGATTCCTTAAAACAACTTGGG	2630	οь
1440	aaggaacaaagggccctgacaacgtaaagacggggatagattccttaaaacaacttgg	1381	Qy
2629	TTTTCCATTGACCCTAATTCGGGTATGAAAAATAAAGGGAAGTATTTGGCTCTTACAGAA	2570	ф

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GENERAL INCOMPATION:
APPLICANT: AMORY, ANTOINE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARA'
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARA'
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARA'
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARA'
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARA'
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESSONDANCE FORM:
ADDRESSEE: WILLIAN BRINKS HOPER GILSON & LIONE, P.C.
STREET: 20006
COMPUTER: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATION
SOFTWARE: PACHOLIAN RELEASE #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1050
TELEFAX: (500 383-5605
INFORMATION FOR SEQ ID NO: 8:
CERCHEMOTE CHARACTERISTICS:
                                                                                                  RESULT 5
US-08-472-293-8
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                                                SEQUENCE CHARACTERISTICS:
LENCTH 4464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-472-293-8
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RESULT 6
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APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARA
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARA
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
RUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSED: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PAtentin Release #1.0, Version #1.25
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEPHONE: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4644 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: TYPE: genomic DNA
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US-08-474-545-8
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Sequence 8, Application US/08474545
PATENT NO. 5736375
GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PRODUCE IT, I
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  MICROORGANISMS WHICH PROCESSES FOR THE PRE
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; TOPOLOGY: linear
: MOLECULE TYPE: genomic
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
Gran NUCLEIC. 4610
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Best Local Similarity
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON STREET: 2000 K Street, N.W., Suite 200 CITY: Washington STATE: D.C.
COUNTRY: U.S.A.
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FILLING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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TYPE: Floppy disk
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; TYPE: nucleic acid
; STRANDEDNESS: sing;
; TOPOLOGY: linear
; MOLECULE TYPE: genom:
US-08-474-545-9
                                                                                                                                                                                                                                                           ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONSTREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/08/474,545
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
REFERENCE/DOCKET NUMBER: 4:21-43
TELECOMMUNICATION NUMBER: 4:21-43
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 4:21-43
TELECOMMUNICATION TOPORMATION:
TELEPAN: (202) 429-6625
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPPE: nucleic acid
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Matches 2793
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APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PRODUCE I
TITLE OF INVENTION: PULLULANA
NUMBER OF SEQUENCES: 15
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RESULT 9
US-08-478-341-8
Sequence 8, Application US/08478341
Patent No. 5817498

GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE AND THE PREPARA'
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, P.C.
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
APPLICATION NUMBER: US/08/478,341
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gaddiano, Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-45
TELEPHONE: (202) 429-0625
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TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
IS-08-478-341-8
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RESULT 10
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                                                                                                                                                                                                  Sequence 9, Application US/08478341
Patent No. 5817498
GENERAL INFORMATION:
      ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LI
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC COMPATIBLE
COMPUTER: HBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                            APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREI
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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APPLICATION
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 NUMBER:
US/08/478,341
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEPHONE: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
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LENGTH: 4464 base pair
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                         CCGAGTTACCCATCTGACAACATTAATTTAACAGTCCCTGCCGGCGGTGCACACGTCACT
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	2761 gtaagcccaggaccacggtaaaaagtaatagaaaa 2794	Qy
4009	GTCAAGCAGAGGGAAGTGTCCAAGTACCAGGTATATCTATGATGATCCTTCATCA	망
2760	l ggtcaagcagagggaagtgtccaagtaccaggtatatctatgatgatccttcatcaaga	Qy
3949	3890 TTGCCGAGCGGGAAATGGGCAATCAATGCTACGAGCGGTAAGGTAGGAGAATCCACCCTT	Ф
2700	41 ttgccgagcgggaaatgggcaatcaatgctacgagcggtaaggtaggagaatccaccct	Qy
3889	3830 GACAAATGGGGAAATATCATTGTTTATAAACCCAAATAAAACTGTAGCAACCATCAAT	B
2640	581 gacaaatggggaaatatcattgttgtttataacccaaataaaactgtagcaaccatcaa	Qy
3829	3770 CAATTCCTAAATAGTCCAGAGAACACAGTGGCCTATGAATTAACTGATCATGTTAATAAA	₽
2580	aattootaaatagtooagagaacacagtggcotatgaattaactgatcatgttaata	Qy
3769	3710 CTTCGTCTTGATCACCCAGCCTTCCGCATGACGACAGCTAATGAAATCAATAGCCACCTC	В
2520	cttcgtcttgatcacccagccttccgcatgacgctaatgaaatcaatagccacct	Qy
3709	3650 GATTGGAGCAGGAAAGCTCAATATCCAGATGTTTTCAACTATTATAGCGGGCTAATCCAC	В
2460	1 gattggagcaggaaagctcaatatccagatgttttcaactattatagcggggctaatcca	Qy
3649	3590 CTTCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAGGCGATGCGGTCAATGAGTTT	타
2400	341 cttcgtanaaaaggcggcaacgacaatagttataatgcaggcgatgcggtcaatgagtt	Qy
3589	3530 GCACAAGCAGTTGTTATGACCTCACAAGGCGTTCCATTCATGCAAGGCGGGAAGAAATG	망
2340	81 gcacaagcagttgttatgacctcacaaggcgttccattcatgcaaggcggggaagaaat	Qy
3529	3470 AAAATAGCCCTAAGCAATCCTAATGATTCCGAAGCGGATCGGATTAAAATGGATGAACTC	망
2280	221 aaaatagccctaagcaatcctaatgattccgaagcggatcggattaaaatggatgaact	Qy
3469	3410 TCTTCACCAGGTGAGACAATTAACTATGTCACAAGTCATGATAACTACACCCTTTGGGAC	DЬ
2220	cttcaccaggtgagacaattaactatgtcacaagtcatgataactacaccctttggga	Qy
3409	3350 GCAACAGGCTTAACTGATGCAATTAAGAATGGCGTTGAGGGGAGTATTAATGACTTTACC	뫄
2160	caacaggcttaactgatgcaattaagaatggcgttgaggggagtattaatgactttac	Qy
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2100	Lacgaaacgcgttggacggcaatgtctttgattcttccgctcaaggttttgcgacagg	Qy
3289	3230 GATCAGCTTCTGACAAAAGGAGCTCAAAAAGGCATGGGAGTAGCGGTGTTTAATGACAAT	ДĎ
2040	atcagcttctgacaaaaggagctcaaaaaggcatgggagtagcggtgtttaatgacaa	Qy
3229	3170 AATCCAGGAATTGCACTTTACGGTGAGGCATGGACGGTGGAACCTCTGCACTGCCAGAT	DЬ
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3169	3110 TTAATGGCGCTGCTTGGAAAAGACACGATGTCCAAAGCTGCCTCGGAGCTTCATGCTATT	DЬ
1920	l ttaatggcgctgcttggaaaagacacgatgtccaaagctgcctcggagcttcatgctat	Ωy
3109	3050 ATTATTGATTCCCTTAAGTATTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGAC	Db

RESULT 11
US-08-996-733-8
; Sequence 8, Application US/08996733
; Patent No. 6074854
; GENERAL INFORMATION:
; APPLICANT: DEWEER, PHILIPPE

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; MOLECULE TY
US-08-996-733-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (650) 845-6504
NFORMATION FOR SEQ ID NO: 8:
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FILING DATE: 28-DEC-17-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09301278
APPLICATION NUMBER: 19-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,293
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,893
FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Debra J. Glaister, Esq.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC446C1-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 23-DEC-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
                                                                                                                       1370 GCTGACTCTTTTGGAGCTGTTGCAAGTGCTGATATTCCAGGAAACCCAAGTCAGGTAGGA 1429
                                                                                                                                                                                                   1250 GATGGGAACACGACAACGATCATTGTCCACTATTTTTGCCCTGGTGATTATCAACCT 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: BE 09300744
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-NOV-PRIOR APPLICATION DATA:
                                                               181 attatcgttcgcactcaagattggaccaaagatgtgagcgctgaccgctacatagattta 240
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  241 agcaaaggaaatgaggtgtggcttgtagaaggaaacagccaaattttttataatgaaaaa 300
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CITY: Palo Alto,
                                                                                                                                                                                                                        61 tggagtctatggatgtggccbaaagacggaggtggggctgaatacgatttcaatcaaccg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 28-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMORY, ANTOINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650) 846-7620
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23-DEC-1997
ЭN Гъргатъ
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28-DEC-1992
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2569	ATTACGCCAAAGAATATAGAAGATGAGGTCATCTATGAAATGGATGTCCGTGAC	2510	ДĎ
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4	CAGGCCAAGGCTCTACCCGAACGGCTGTTGATCCTTATGCAACTGCGATTGCACCAAAT	39	рь
1200	caggccaaggctctacccgaacggctgttgatccttatgcaactgcgattgcaccaaa	1141	Qy
ü	GTGTGTGGGAAGCAACGGTTAATCAAAACCTTGAAAATTGGTATTACATGTATGAGGTA	2330	Db
1140	gtgtgtgggaagcaacggttaatcaaaaccttgaaaattggtattacatgtatgaggta	1081	у
2329	ACCTATGACGGCATCGGGCCAT	2270	Db
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2269	TGTTCTT	2210	Db
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2209	TACCTAT	2150	DЪ
960	taatgtgcttaattcatcaccagtactactattcaggagatgatcttgggaatacctat	901	Qy
2149	GAGCCATACTCTGTCCATTCAAACAGATGGCTATCAGGCAAAGCAGGTGATACCT	2090	Db
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2029	CCTAATGCGGAT	1970	Db
780	tttcgtatattccgtccactcatgcagtctatgacacaattaataatcctaatgcgga	721	γQ
1969	GTGCACACG	1910	Db
720	cyagitacccaictgacaacaitaaittaacagicccigccggcggigcacacgicac	661	Qy
1909	GAGATCTTCCTGAAGGAAACTACCAATATAAAGTGGCTTTAAATGATAGCTGGAATAAT	1850	DЪ
660	gagatottootgaaggaaactaocaatataaagtggotttaaatgatagotggaataat	601	Qy
1849	GCACCTGATAATCACAGTACTTTATTAAAAAAGGTGACTAACAATCTCTATCAATTCTCA	1790	ФФ
600	cacctgataatcacagtactttattaaaaaaggtgactaacaatctctatcaattctca		Оу
1789	CAAGATGTAACCGCTGTTTTGGCAGGTACCTTCCAACATATTTTTGGAGGTTCCGATTGG	1730	DЪ
540	angatgtaaccgctgttttggcaggtaccttccaacatatttttggaggttccgattgg	481	Оу
1729	CATGACGACAGCAAATAAGGATATTCCAGTGACATCTGTGAAGGATGCAAGTCTTGGT	1670	Db
480	atgacgacacagcaataaggatattccagtgacatctgtgaaggatgcaagtcttggt		Оу
1669	GTGCTGGTTAAACTTAGCCAGCCGTTAACTCTTGGGGAAGGNNNAAGCGGCTTTACGGTT	1610	Db
420	tgctggttaaacttagccagccgttaactcttggggaaggnnnaagcggctttacggt	w	Оу
1609	GATGCTGAGGATGCAGCTAAACCCGCTGTAAGCAACGCTTATTTAGATGCTTCAAACCAG	1550	рb
	algolyaggalgoagolaaaccogolglaagcaacgollattlagalgolloaaaccag		ογ
1549	AGCAAAGGAAATGAGGTGTGGCTTGTAGAAGGAAACAGCCAAATTTTTATAATGAAAAA	1490	Db

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APPLICATION UNBER: US/08/996,733
FILING DATE: 23-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,293
PRIOR APPLICATION OF THE PRICE O
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, V. CURRENT APPLICATION DATA:
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APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE,
TITLE OF INVENTION: PRODUCE IT, P
TITLE OF INVENTION: PULLULANASE A
NUMBER OF SEQUENCES: 15
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ADDRESSEE: Genencor International,
STREET: 925 Page Mill Road
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TELEFAX: (650) 845-6504
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
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aatccaggaattgcactttacggtgagccatggacgggtggaacctctgcactgccagat
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RESULT 13
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                                     APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREE
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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ADDRESSEE: WILLIAN BRINKS HOFER GILSON STREET: 2000 K Street, N.W., Suite 200 CITY: Washington
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-474-140-10
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Best Local Similarity
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COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
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APPLICATION NUMBER: US/08/4
PILING DATE: 07-JUN-1995
PILING PATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gaddano, E
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STREET: 2000 K Street, N.W., Suite 2
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC LOSS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT HOPOMATION:
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TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON
2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
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APPLICANT: AMORY, ANTOINE
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STRANDEDNESS: sing
TOPOLOGY: linear
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Local Similarity
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(202) 293-1850
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MEDIUM TVER: FLORY
MEDIUM TVER: FLORY
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/88/472,293
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-1850
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDENMESS: single
                                                                                      TOPOLOGY: 1;

MOLECULE TYPE:
US-08-472-293-10
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 Query Match
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Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: WILLIAN BRI
STREET: 2000 K Street,
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
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Title: Perfect score:

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GENERAL INFORMATION:
APPLICANT: Miller, Brian S.
APPLICANT: Shetty, Jayarama K.
TITLE OF INVENTION: Modified Forms of Pullulanase
FILE REFERENCE: GC396-2
CURRENT APPLICATION NUMBER: US/09/262,126C
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2794
                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Bacillus deramificans
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2794)
; OTHER INFORMATION: n = A, T, C, o
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Result No.

Score

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Database

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6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 su

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of hits satisfying chosen parameters:

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; NAME/KEY: misc_feature; LOCATION: (2641); OTHER INFORMATION: n = a or US-09-463-238-2
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Best Local Similarity
Matches 164; Conserv
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CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Starch Debranching Enzymes FILE REFERENCE: 97.118
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Plant Bioscience Limited
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Pred. No. 3.6e-05;
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NAME/KEY: misc_feature

LOCATION: (822, 826, 2707 and 2797)

OTHER INFORMATION: n = a or g or c or US-09-463-238-11
                                                                                         APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1998-07-31
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LENGTH: 2806
TYPE: DNA
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Best Local Similarity
Matches 89; Conserv
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CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
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NUMBER OF SEQ ID NOS: 30 SOFTWARE: PatentIn Ver. 3EQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: GB 9716185.5 PRIOR FILING DATE: 1997-07-31 NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Edwards, Elizabeth A
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Martin, Catherine R
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Pred. No. 0.0034;
0; Mismatches 74;
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Sequence 3, Application US/09463238

SEQUENCE 1 INFORMATION:

APPLICANT: Edwards, Elizabeth A

APPLICANT: Smith, Alison M

APPLICANT: Bustos Guillen, Regla

APPLICANT: Hartin, Catherine R

APPLICANT: Plant Bioscience Limited

TITLE OF INVENTION: Starch Debranching Enzymes

FILE REFERENCE: 97.118
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 10
LENGTH: 2843
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Best Local Similarity
Matches 67; Conserv
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Best Local Similarity
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APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
APPLICANT: Martin, Catherine R
APPLICANT: Plant Bloscience Limited
APPLICANT: Plant Bloscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/GB98/02280 PRIOR FILING DATE: 1998-07-30 PRIOR APPLICATION NUMBER: GB 9716185.5
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CURRENT FILING DATE: 2000-01-21
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TYPE: DNA
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Pred. No. 0.16;
0; Mismatches 48;
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; PRIOR APPLICATION NUMBER: GB 9716185.5; PRIOR FILING DATE: 1997-07-31; NUMBER OF SEQ ID NOS: 30; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 3; SEQ ID NO 3; LENGTH: 2634; TYPE: DNA; ORGANISM: SOlanum tuberosum US-09-463-238-3
RESULF 8
US-60-248-505-164
Sequence 164, Application US/60248505
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: (1)...(264546)
; OTHER INFORMATION: n - A
US-60-248-505-202
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LENGTH: 264546
TYPE: DNA
ORGANISM: human
FEATURE:
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APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: cl000918
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Best Local Similarity
Matches 53; Conserv
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Best Local Similarity 51.6%;
Matches 82; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-11-15
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CURRENT FILING DATE: 2000-01-21
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                                                                                                                                34150 aaaactaataagtgagtttatcagggttgcagacaagat 34188
                                                                                                                                                                                                                     34090 ctggcagatgatatgcttatgtcatttatctgaaaaatcagagtttaccaaaaagatagt 34149
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                                                                                                                                                         1501 acccaagataattygygttatyaccctcgcaactatyat 1539
                                                                                                                                                                                                                                                1441 attactcatgttcagcttatgcctgttttcgcatctaacagtgtcgatgaaactgatcca 1500
                                                                                                                                                                                                                                                                                                                                   1381 aaaggaacaaagggccctgacaacgtaaagacggggatagattccttaaaacaacttggg 1440
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; Pred. No. 24;
0; Mismatches
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NAME/KEY: misc_feature

: LOCATION: (1)...(133937)

: OTHER INFORMATION: n = A,T,C

US-60-248-822-8
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; ORGANISM: human
US-60-248-505-164
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                                                                        В
                                                                                                                                               Db 120075 ttctggaggttaggaagcttagaaggtgaatggttatcaacttttacaatagttttaaca
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TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN
TITLE OF INVENTION: RECEPPORS, NUCLEIC ACTI
TITLE OF INVENTION: PROTEINS, AND USES THEI
FILE REFERENCE: c1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
LENGTH: 133937
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/60248822
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 164
LENGTH: 91051
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Best Local :
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CURRENT FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 30
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 120195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                            1602 aatggttctttcactccatcgtgaacacattggggttaacatggatgttgtctataatca 1661
                                                                                                                                                                    1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1379 aaaaaggaacaaagggccctgacaacgtaaagacgggggatagattccttaaaacaacttg 1438
                                     1662 tac 1664
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Local Similarity 49.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caacccaagataattggggttatgaccctcgcaactatgatgttcctgaagggcagtat 1557
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tac 120197
                                                                        aagagtttattttatcaaaattacacacggcaaaaaatacaatgctatttcattttacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           catcctattgtcttttattttgtgtccttgggctataaaagattcctgaatgtaattat 89729
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ISOLATED HUMAN G-PROTEIN COUPLED
PROTEIN COUPLES ENCODING HUMAN GPCR
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                                                                                                                                                                                                                                           1.30;
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                                                                                                                                                                                                                                           Score 35;
Pred. No.
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                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                           DB 6; Length 133937; 28;
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Sequence 127, Application US/60248505

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCORPTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: C1000918

CURRENT APPLICATION NUMBER: US/60/248,505

CURRENT FILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 1998

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 127

LENGTH: 22788
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NAME/KEY: misc_feature
; LOCATION: (1)...(2794)
; OTHER INFORMATION: n -
US-09-262-126C-1
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US-09-262-126C-1/c
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; NAME/KEY: misc_feature
; LOCATION: (1)...(22788)
; OTHER INFORMATION: n =
US-60-248-505-127
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TITLE OF INVENTION: Modified forms of Pullulanase
FILE REFERENCE: GC396-2
CURRENT APPLICATION NUMBER: US/09/262,126C
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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Best Local Similarity
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                                                                                      FEATURE:
                                                                                                       ORGANISM: human
                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2426 GGATATTGAGCTTTCCTGCTCCAATCAA 2399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atttgccgagcgggaaatgggcaatcaa 2666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGAAGGCTGGGTGATCAAGACGAAGGTGGATTAGCCCGCTATAATAGTTGAAAAACATCT 2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aagacaaatggggaaatatcattgttgtttataacccaaataaaactgtagcaaccatca
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                      A,T,C
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SEQUENCE 354, APPINICATION US/60248505

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID
TITLE OF INVENTION: PROTEINS, AND USES THER
FILE REFERENCE: C1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 354
LENGTH: 55248
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; ORGANISM: human
US-60-248-505-611
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TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: C1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 611
LENGTH: 30167
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%;
Best Local Similarity 60.0%;
Matches 57; Conservative
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                                                                            TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17167 AAAGTGCCATCCTTAAAAAGTTATTTCTAAATTCTGTAAGTTTTTGTTCAATGTGTGAC 17108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15781 ATCCTTGTTCCTGATCTTAGAGGAAATGTTTAAACTTTTCATTCTTGCAAATGAT 15722
NAME/KEY: misc_feature LOCATION: (1)...(55248) OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15721 GTTAGCAGTGGGCTTGTGATTTATGGCTTTATGATTCTGTACCTAATTTGTTTTAGAATTT 15662
                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15661 TCATTATCAAAGGAATTGTATTAAATGCCTTTTTCAGAATCTATTGAAATATTCTA 15607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1838 atattgacggcttccgttttgacttaatggcgctg 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1778 aaaggccaatggttcaaaaatttatttattgattcccttaagtattgggtcaatgagtatc 1837
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                       (55248)
                                                                                                                                                                                                                                                                ISOLATED HUMAN G-PROTEIN COUPLED
RECEPTORS, NUCLEIC ACID MOLECULES ENCODING
PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%;
    A,T,C
    or
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Pred. No. 17;
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Pred. No. 20;
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; FEATURE:

NAME/KEY: misc_feature

: LOCATION: (1)...(150471)

: OTHER INFORMATION: n - A

US-60-248-505-148
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; ORGANISM: human
US-60-248-505-254
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US-60-248-505-254/c
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                                                                                                                                                                                                                                        Sequence 148, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REPERENCE: C1000918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 254, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: C1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
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SOFTWARE: FastSEQ for
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Best Local Similarity
Matches 72; Conserv
                                                                                                                                                  SOFTWARE: FastSEQ
SEQ ID NO 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                         LENGTH: 150471
TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52084 AAAAAAAAGGGTCAAATATGCTCTTTTAGATATTGCAGTATGAAAATCTGTAAATTAAAATC 52025
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nes 57; Conservative
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Copyright (c) 1993 - 2000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Match Length DB		ID	Description
_ ;	49.6	1.8	874	119	AW727770	AW727770 GAEa002
2	45.6	1.6	974	225	AZ673433	AZ673433 ENTIK90TH
ω	45	1.6	578	167	BE493792	
4	44.2	1.6	1201	229	CNS0168L	•
ი 5	43.4	1.6	1101	229	CNS0039G	_
6	۵	1.5	373	202	AQ100007	7
7	42.8	1.5	558	174	BG227648	œ
ი 8	42	1.5	644	24	A1737641	
9	40.B	1.5	612	167	BE444461	BE444461 WHE1111_F
10	39.8	1.4	365	118	AW697292	
c 11	39.8	1.4	532	150	BF587295	
12	39.8	1.4	921	119	AW730507	၇ ရ
c 13	39.6	1.4	893	223	AZ532406	Ċν
c 14	39.6	1.4	920	225	AZ683014	-
15	39.6	1.4	923	225	AZ668671	_
16	39.2	1.4	558	120	AW832588	В
c 17	39.2	1.4	912	223	AZ549196	Ç
18	39	1.4	611	110	AW034518	_

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                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clemson University
100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Wing RA
                                                                                                                                                                                                                                                       Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                            Gossypium arboreum.
Gossypium arboreum
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EST.
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AW727770 AW727770
                                                                                                                                                        Email: rwing@clemson.edu
High quality sequence sto
                                                                                                                                                                                                                       Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                              Malvales;
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            ø
                                                    /db_xref="taxon:29729"
/clone="GA_Ea0078A17"
/clone_lb-"Gossyplum arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                     /lab_host="E, coli"
/note="Vector: pBK-
                                                                                                           /organism="Gossypium arboreum"
/strain="AKA"
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                                                                                                 /cultivar-"8400"
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AW506191
BE870915
           :: pBK-CMV; Site_1: EcoRI; Site_2: xhoI*
225 g     261 t     2 others
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AZ538451
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AQ280563 CITBI-E1-
AQ280703 CITBI-E1-
AQ287730 CPG2620A
AQ287730 CPG2620A
AZ676090 ENTLQ90TR
AZ680209 ENTMB60TR
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Location/Qualifiers
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Seq primer: M13-Reverse
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Clones are derived from
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
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Anderson,O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J., Fento,R.D., Gustafson,J.P., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the whea genomes - Anther cONA library from rye unpublished (2000)
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BE493792 BE493792.1 GI:9660385
                                                                                                                                                                  Contact: Olin Anderson
US Department of Agriculture, Agriculture R
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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                                                                                                           Email: oandersn@pw.usda.gov
Scquence have been trimmed
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/organism="Secale cereale"
/cultivar="Blanco"
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                                                                                                                                                                                                   Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNS0168L 1201 bp DNA GSS 26-JUL-1 Drosophila melanogaster genome survey sequence SP6 end of BACN15C22 of DrosBAC library from Drosophila melanogaster fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone="WHE1275_E05_109"
/clone_lib="Secale cereale anther cDNA library"
/clone_lib="DrosBAC"
/clone="BACN15C22"
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/dev_stage="Adult plant before anthesis"
/lab_host="E. coli SOLK"
                                                    /db_xref="taxon:7227"
                                                                             /organism-"Drosophila
/plasmid-"pBeloBAC11"
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                                       The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

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                                    Sequence-tagged connectors: scanning the human genome Proc. Natl. Acad. Sci. U. S.
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HS_3054_B1_F07_MF CIT Approved Human Genomic Sperm Library
Saplens genomic clone Plate-3054 Col-13 Row-L, DNA sequence
Contact: Mahairas
                       99380589
                                                                                                                     Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Local Similarity 50.2%;
hes 106; Conservative
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3054 row: L column: 13
Class: BAC ends
High quality sequence stop: 373.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGGAAGAAGAGAGATAATAAAGAAAAGAAGAATGACTAGAAAAAGAAGGATGT
                                                                                                                                                                            McCarter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Undorwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                           Strongyloides stercoralis
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagroialmoidea; Strongyloididae; Strongyloides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG227648 . 558 bp mRNA EST 08-FEB-2001 kq13el0.yl TBN957M-SSR Strongyloides stercoralis cDNA 5' similar WP:T10F2.1 CE02040 GLYCYL-TRNA SYNTHETASE ;, mRNA sequence. BG227648 GI:12715282
                                           Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                            The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
    The library was constructed by Dr. NIAID, NIH (tnutman@nih.gov). DNA S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center 
University of Washington
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E-Coll DH10B"
1 36 c 67 g 120 t
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 0.31;
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  and colleagues
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RESULT 8
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AUTHORS
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Matches 125
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Stanford University
855 California Ave, Palo
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI737641 644 bp mRNA EST 02-FEB-20 605036B10.x2 605 - Endosperm cDNA library from Schmidt lab
                                                                                                                        Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                          Zea mays
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                                                                                                Department of Biological Sciences
                                                                                                                                                                          University
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/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
ECORI; Site_2: XhoI; mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. cDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the ECORI site to the XhoI site. The library
has an unamplified titer of 1 x 10E5 pfu/ml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              average insert size of the unamplified library is 675 bp (range, 100-1700)."
71 c 100 g 182 t
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/strain="Rhabditliform larvae obtained
/db_xref="taxon:6248"
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                                                                                                                                                                                                cDNA libraries
                                                   Alto, CA 94304, USA
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Best Local Similarity
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Mamnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE444461 612 bp mRNA EST 25-JUL-2000 WHE1111_H10_P19ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1111_H10_P19, mRNA
                                                                                                                              quality sequence with phred score less Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                        800 Buchanan Street,
Tel: 5105595773
                                                                                                                                                                                                                                       genomes - Normalized root cDNA library Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                  Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhan The structure and function of the expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                    Sequence have been trimmed to remove vector
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                                                                                                                                                                                   Email: oandersn@pw.usda.gov
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605036 row: B col
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/organism-"Triticum aestivum"
/cultivar-"Chinese Spring"
/db_xref-"taxon:4565"
/clone-"WHEIl11_H10_P19"
/clone_lib-"Wheat etiolated s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Site_2: XhoI; Kernel endosperm
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/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: Kernel; Vector: pAD-GAL4-2'; Site_1:
Site_2: XhoI; Kernel endosperm cDNA library from So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/cultivar="Ohio43"
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Pred. No. 0.75;
0; Mismatches
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Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
, Tong,J.C. and Zhang,D.
   etiolated seedling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggggaagaaatgcttcgtanaaaaggcggcaacgacaatagttataatgcaggcgatgcg 2388
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                                                                                                                                                                                     Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.

1 (bases 1 to 365)
He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell
He, X.-Z., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
                                                                     Unpublished (2000)
On Apr, 14, 2000 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NF117C04ST1F1033 Developing stem Medicago NF117C04ST 5', mRNA sequence.
  Plant Biology Division
The Samuel Roberts Nob
                                                 Contact: Dixon
                                                                                                                    Expressed Sequence Tags from the Medicago truncatula stem library
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                                                                                                                                                                      , R.A.
                                                                                                                                                                                                                                                                                                                                                              barrel medic.
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  Samuel Roberts Noble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-*Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystalization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TI Close lab (Choi, Close, Fenton) at the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DHIOB"
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Pred. No. 1.
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Foundation
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                         Department of Botany
The University of Georgia
Plant Sciences Building, Rm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorghum propinquum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
                                                                                                                                                                                                                              Email: mmpratt@uga.cdu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequences
                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF587295 532 bp mRNA
FM1_34_F08.b1_A003 Floral-Induced
                                                                                                                                                                                            Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                           An EST database from Sorghum: floral-induced meristems
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cordonnier-Pratt, M.-M., Gingle, A.,
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BF587295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: radixon@noble.org
Insert Length: 778 Std Error: 0.(
Plate: 117 row: C column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
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706 542 1805
                                                                                                                                                                          quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="NF117C04ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture
internodal stem segments"
1 65 c 95 g 110 t
             /organism="Sorghum propinquum"
/db_xref="taxon:132711"
/clome_lib="Floral-Induced Meristem 1 (FML)"
/note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI;
EcoRI; mature plants were placed in a growth chamber
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/db_xref="taxon:3880"
                                                                                                                                       Location/Qualifiers
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61.4%;
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Meristem 1 (FM1) Sorghum
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Best Local Similarity 49.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101;
                                                                                                                                                                                                                                                                                                                                                                                                                   ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber Unpublished (2000) Contact: Wing pa
                                                                                                                                                                                                                                                                                                                                                                    Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GA_Ea0026B23 Gossyplum arboreum 7-10 dpa fiber library Gossyplum arboreum CDNA clone GA_Ea0026B23, mRNA sequence.

AW730507
                                                                                                                                                                                                                                                                                                              100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gossypium arboreum
                                                                                                                                                                                                                                                                     High quality sequence stop:
                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gossypium arboreum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW730507.1 GI:7628151
    256
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    a
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                                                                                 /db_xref="taxon:29729"
/clone="GA_E80026B23"
/clone_ilb-"Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
160 c 239 g 266 t
                                                                                                                                                                                      organism="Gossypium arboreum"/strain="AKA"
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                       /cultivar-"8400"
                                             lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                       Clemson,
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Pred. No. 3;
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153; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ532406 DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA library
Seq primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bjloftus@tigr.org
Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Entamoebidae; Entamoeba
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                                                                                                                                                                                                                                                                                                                                                                           quality sequence start: 22 quality sequence stop: 812. Location/Qualifiers
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                          /Clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
/note "Vector: pHOS1; Site_l: Bst I; Constructed at The
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/note "Vector: pHOS1; PHOS1;
77:450.). The DNA was mechanically sheared to
                                                                                                                                                                                                                                                                                  /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
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Pred. No. 3.
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Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Entamoeba histolytica HM1:IMSS sheared
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ENTHN79TR Entamoeba
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High quality sequence start:
High quality sequence stop:
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Clones are derived from the
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Contact: Brendan J Loftus
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The Institute for Genomic Research
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                                                                                                                                            /Clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/nstitute for Genomic Research (TIGR), Rockfille, MD
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
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method for isolate identification. Exp. parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
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Pred. No. 4.2;
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whole genome shotgun sequencing

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Class: shotgun
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Clones are derived from the Entamoeba histolytica HMl:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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          /clone_lib="Entamceba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Constructed at The
/note="Vector: pHOS1; Site_1: Constructed at The
/note: Institute for Genomic Research (TIGR), Rockville, MD.

Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
/7:450,). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
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Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Copyright (c) 1993 - 2000 Comp
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Pullulanase amino Bacillus deramific Bacillus deramific Trimmed enzyme pro Pullulanase (pulB) Thermotoga maritim Thermotoga maritim Fervidobacterium p
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Y06918 Y04387	P90615	B05950	W36602	Y17523	Y34991	Y37184	Y78515	W95636	Y78516	P94419	Y50819	Y00872	Y00870	W53885	R92692	W53886	R92693	Y00869	W35390	W55098	W34878	Y27357	W09257	W73552	Y91279	P82507	37	W81973	2	55	161	R23787
Partial hexaploid Pullanase type par	ide with	otein dedu	tuberosum	a mays SUl s		10	Isoamylase amino a	Rhodothermus marin	Isoamylase amino a	Primary transcript	Wheat isoamylase p	-		_	isoamylase precurs		S	S. tuberosum isoam	lavobacterium	reptoc	ΥS		Bacillus alkaline	lan	Group B Streptococ	llul	ach	n pull	illus alk	Full length Pullul	Thermostable pullu	Heat-resistant pul

ALIGNMENTS

RESULT R56990

Bacillus deramificans pullulanase precursor.

21-FEB-1995 (first entry)

R56990;

R56990 standard; Protein; 957 AA

/note- "corresponds to GCN codon" Misc-difference 812 /note= "corresponds to CAN codon" Misc-difference 621 /note- "corresponds to NNA codon" Misc-difference 620 /note= "corresponds to GGN codon" Misc-difference 164 Location/Qualifiers Bacillus 28-DEC-1992; 20-DEC-1993; 06-JUL-1994. EP605040-A. hydrolysis; alpha-1,6-glycosidic bond; starch saccharification Pullulanase; recombinant production; pullulan; amylopectin; deramificans T 89.117D (LMG P-13056). 92BE-0001156 93EP-0203593 /note= "corresponds to ANA codon"

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Query Match
Best Local :
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                              PYATAIAPNGTRGMIVDLAKTDPAGWNSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKN
                                                                                                                                                                                                           VTVTLGEDPDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWA
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                                                                                                                                                                     PTSTQVNVLLYDSATGSVTKIVPMTASGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVD
                                                                                                                                                                                                 vtvtlgedpdvshtlsiqtdgyqakqv1prnvlnssqyyysgddlgntytqkattfkvwa
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93BE-0001278.
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DNA vectors, transformed cells etc.
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pred. No. 0; 
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New modified pullulanase

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                                                  (GEMV ) GENENCOR INT INC
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1999-540851/45.
DB; X87941.
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                                                                                                                                                                                                                                                                                                                                                                       ase; enzyme engineering; starch; saccharification; chain amylase; alpha-dextrin 6-glucano-hydrolase;
                             Shetty JK;
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of Claim 31
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(see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents Bacillus deramificans strain TR9.117D mature pullulanase (EC-3.2.1.41). This enzyme has a pI of CC 4.1.4.5, has a half-life of about 55 hr at 60 deg C and is capable CC of catalysing the hydrolysis of alpha-1.6-glucosidic bonds in CC amylopectin and pullulan. The invention relates to the discovery CC that B. deramificans pullulanase recombinantly produced in a Bacillus host is modified yet retains the ability to catalyse the CC hydrolysis of an alpha-1.6-glucosidic bond. The modification of CC the recombinant pullulanase appears to be a result of misprocessing CC of the signal sequence by a signal peptidase as well as CC susceptibility to extracellular proteolytic processing. The CC invention provides modified pullulanases, especially N-terminally CC truncated B. deramificans modified pullulanase (see Y31747-48), CC nucleic acids encoding them, vectors, host cells and methods for CC recombinant production. The modified pullulanase sare useful in CC the starch industry for the saccharification of aqueous liquefied CC starch, forming syrups of high glucose and maltose content. Other CC uses (not claimed) are: as anti-staling additives in bread; in CC tertaholosides from maltose; to condense monor or of of other cCC amylose is used as substitute for fat); to clarify fruit juices; CC in the preparation of oligosaccharides from amylopectin or of tertaholosides from maltose; to condense monor or oligosaccharides, cc or in the pharmaceutical industry (no details). When used for Starch saccharification, the modified pullulanases reduce the amounts of by-products, especially they provide higher glucose CC reversion reaction products. When used with glucoamylase, they can be considered and productivity and a more central process.
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Local Similarity 99.9%;
les 927; Conservative
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                            KHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLG
                                                         gvweatvnqnlenwyymyevtgqgstrtavdpyataiapngtrgmivdlaktdpagwnsd
                                                                                                                        rnvlnssqyyysgddlgntytqkattfkvwaptstqvnvllydsatgsvtkivpmtasgh
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Misc-difference 592
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Misc-difference 591
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93BE-0000744.
93BE-0001278.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the mature pullulanase enzyme isolated from Bacillus deramificans T 89.117D. The pullulanse hydrolyses alpha-1,6-glycosidic bonds of amylopectin and of pullulan. The enzyme can be used (with glucoamylase) for saccharification of starch. Typical applications include use as anti-staling additives in bread making and brewing, in preparation of low calorie foods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New pullulanase from saccharification etc. ranges, also related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 4;
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d@lltkgaqkgmgvavfndnlrnaldgnvfdssaqgfatgatgltdaikngvegsindft
         DQLLTKGAQKGMCVAVFNDNLRNALDGNVFDSSAQGFATGATGLTDAIKNGVEGSINDFT
                                       ITHVQLMPVFASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLH
                                                                                                                                                                            khitpkniedevlyemdvrdfsidpnsgmknkgkylaltekgtkgpdnvktgidslkqlg
                                                                                                                                                                                        KHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLG
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926; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 4888.5;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                         Pullulanase; debranching enzyme; amylopectin; thermostable; corn; genetically engineered variant; wheat; potato; wheat; manioc; rice starch; sugar production; high fructose syrup; high maltose syrup;
                                                                                                                                       Claim
                                                                                                                                                           Variant bacterial pullulanases and isoamylases having, e.q thermostability, used for converting starch from potatoes
                                                                                                                                                                                               Bisgard-Frantzen H,
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                                                                                                                                                                                                                             02-JUL-1998;
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                                                                                                                                                                                                                                                                                     Bacillus deramificans
                                                                                                                                                                                                                                                                                                                                       Pullulanase
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This sequence represents a pullulanase amino acid sequence. Pullulanases CC are debranching enzymes which can attack amylopectin. This sequence represents a parent enzyme from which genetically engineered variant compresents a parent enzyme from which genetically engineered variant compresents apparent enzyme from which genetically engineered enzyme has an improved thermostability at a pH in the range of 4-6 compared to the comparent enzyme. The modified enzyme may alternatively or also have an increased activity towards amylopectin and or glycogen compared to the comparent enzyme. This is useful when starches such as corn, potato, wheat, compared to the corner sugars. This is useful when starches such as corn, potato, wheat, compared to the corner sugars. This is useful when starches such as corn, potato, wheat, compared to the corner sugars, such as high fructose syrup, high maltose syrup, maltodextrins, amylose, 64-66 oilgosaccharides and other coarbonydrates such as fat replacers. The thermostable debranching enzymes of the invention make it possible to perform liquefaction and debranching the thermostable debranching using the thermostable debranching using the thermostable debranching using the thermostable debranching the pancer of pance precursors with the action of an alpha-amylase, the formation of pance precursors ciscustable debranching enzyme variants during liquefaction together with the action of an alpha-amylase, the formation of pance precursors.

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                                                                                                                                             DGNTTTIIVHYFCPAGDYQPWSLWMWPKDGGGAEYDFNQPADSFGAVASADIPGNPSQVG 89
                                                                       OLGITHVQLMPVFASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVL
                                                                                                                                                                                                                                                                                                       NSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLK 505
                                                                                                                                                                                                                                                                                                                                           SGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGW
                                                                                                                                                                                                                                                                                                                                                                     viprnvlnssqyyysgddlgntytqkattfkvwaptstqvnvllydsatgsvtkivpmta
                                                                                                                                                                                                                                                                                                                                                                              VIPRNYLNSSQYYYSGDDLGNTYTQKATTFKYWAPTSTQVNYLLYDSATGSYTKIVPMTA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                           apdnhstllkkvtnnlyqfsgdlpegnyqykvamshs---aqpvtsvqavwpgrpyplga
                                              SHLQFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGE
                                                                                                                                                                                 qlgithvqlmpvfasnsvdetdptqdnwgydprnydvpegqyatnangnarikefkemvl
                                                                                                                                                                                                                                                                                                                                  sghgvweatvnqnlenwyymyevtgqgstrtavdpyataiapngtrgmivdlaktdpagw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINLTVPAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dgntttiivhyfrpagdyqpwslwmwpkdgggaeydfnqpadsfgavasadipgnpsqvg 60
        STLGQAEGSVQVPGISMMILHQEVSPDHGKK 956
                                                                                                                                                                                                    OKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSA
                                                                                                                                                                                                                                                                                              nsdkhitpkniedeviyemdvrdfsidpnsgmknkgkylaltekgtkgpdnvktgidslk
stlggaegsvqvpgismmilhqevspdhgkk 915
                                    <u>shlqflnspentvayeltdhvnkdkwgniivvynpnktvatinlpsgkwainatsgkvge</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              866;
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93.0%;
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Pred. No. 6.3e-297;
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RESULT
Y31747
 pullulanase of Bacillus deramificans strain T89.1170, comprising CC amino acids 99-928 of the native mature enzyme (see Y31746). The cannot acids 99-928 of the native mature enzyme (see Y31746). The CC native mature pullulanase (EC-3.2.1.41) has a pI of 4.1-4.5, a CC half-life of about 55 hr at 60 deg C and is capable of catalysing CC the hydrolysis of alpha-1,6-glucosidic bonds in amylopectin and cc pullulan. The invention relates to the discovery that B. CC deramificans pullulanase recombinantly produced in a Bacillus host CC is modified yet retains the ability to catalyse the hydrolysis of CC an alpha-1,6-glucosidic bond. The modification of the recombinant CC pullulanase appears to be a result of misprocessing of the signal CC sequence by a signal peptidase as well as susceptibility to extracellular proteolytic processing. The invention provides CC modified pullulanases, especially N-terminally truncated B. CC deramificans modified pullulanase, nucleic acids encoding them, CC vectors, host cells and methods for recombinant production. The condified pullulanases are useful in the starch industry for the saccharification of aqueous liquefied starch, forming syrups of CC anti-staling additives in bread; in brewing low calorie beers; CC anti-staling additives in bread; in the processis used as substitute CC carefity for first the vices: in the preparation of
industry
modified
                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an N-terminally truncated pullulanase of Bacillus deramificans strain T89.117D, com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAR-1999;
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Misc-difference 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified pullulanase for saccharification of aqueous liquefied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pullulanase;
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                                             for fat); to clarify fruit juices; in the preparation of oligosaccharides from amylopectin or of tetraholosides f
            to condense mono- or oligosaccharides, or in the pharmaceutical industry (no details). When used for starch saccharification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-540851/45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme engineering;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0034630
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783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-truncated pullulanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "encoded by NNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "encoded by GGN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "encoded by CAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρλ
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                                              from maltose;
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Best Local
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Note: The present sequence is not shown in the specification but is derived from the B. deramificans pullulanase sequence given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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INLPSGKWAINATSGKVGESTLGQNEGSVQVPGISMMILHQEVSPDHGKK 956
                                                  IHLRLDHPAFRWTTANEINSHLQFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVAT
                                                                                                        elaqavvmtsqgvpfmqggeemlrxkggndnsynagdavnefdwsrkaqypdvfnyysgl
                                                                                                                                                                            TGATGLTDAIKNGVEGSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMD
                                                                                                                                                                                                                   ainpgialygepwtggtsalpddglltkgaqkgmgvavfndnlrnaldgnvfdssaqgfa
                                                                                                                                                                                                                                 AINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFA
                                                                                                                                                                                                                                                                       iiptdqvlemklxaerpmvqkfiidslkywvneyhidgfrfdlmallgkdtmskaaselh
                                                                                                                                                                                                                                                                                    IIPTDQVLEMKLXAERPMVQXFIIDSLXYWVNEYHIDGFRFDLMALLGKDTMSKAASELH
                                                                                                                                                                                                                                                                                                                          y at nangnarlke fkemvlslhrehigvn m dvvynhtfat qisdfd kivpeyyyrt miqv\\
                                                                                                                                                                                                                                                                                                                                        YATNANGNARIKEFKEMYLSLHREHIGVNMDVYYNHTFATQISDFDKIVPEYYYRTMIQV
                                                                                                                                                                                                                                                                                                                                                                              PNGTRGMIVDLAKTDPAGWNSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dpdvshtlsiqtdgyqakqviprnvlnssqyyysgddlgntytqkattfkvwaptstqvn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTEKVWAPTSTQVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NN-SYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                    pngtrgmlvdlaktdpagwnsdkhitpkniedevlyemdvrdfsidpnsgmknkgkylal
                                                                                                                                                               tgatgltdalkngvegsindftsspgetinyvtshdnytlwdkialsnpndseadrikmd
                                                                                                                       829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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99.9%;
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Pred. No. 2.5
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as substitute from maltose;

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RESULT
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modified pullulanases, especially N-terminally truncated B.

deramificans modified pullulanase, nucleic acids encoding them,
vectors, host cells and methods for recombinant production. The
modified pullulanases are useful in the starch industry for the
saccharification of aqueous liquefied starch, forming syrups of
high glucose and maltose content. Other uses (not claimed) are: as
anti-staling additives in bread; in brewing low calorie beers;
production of low calorie foods (where maylose is used as substitute
for fat); to clarify fruit juices; in the preparation of
oligosaccharides from amylopectin or of tetraholosides from maltose;
to condense mono- or oligosaccharides, or in the pharmaceutical
industry (no details). When used for starch saccharification, the
modified pullulanases reduce the amounts of by-products, especially
they provide higher glucose yields in short reaction times, without
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Misc-difference 591
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified pullulanase for saccharification of aqueous liquefied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-540851/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme engineering; starch; saccharification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0034630
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Best Loc
Matches
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Note: The present sequence is not shown in the specification but is derived from the B. deramificans pullulanase sequence given in
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Local Similarity 99.2
-- 825; Conservative
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                                                                                                                                                                               GIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATGAT
                                                                                                                                                                                                                                                                                          DSATGSVTKIVPMTASGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                VTAVLAGTFQHIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNN-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKDASLGQD
GLTDAIKNGVEGSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQ
                                                                                                                                                                                                                                                                                                                                                                 shtlsiqtdgygakqviprnvlnssqyyysgddlgntytqkattfkvwaptstqvnvlly
                                                                                                                                                                                                                                                                                                                                                                          SHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                      vtavlagtfqhifggsdwapdnhstllkkvtnnlyqfsgdlpegnyqykvalndswnnps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           edaakpavsnayldasnqvlvklsqpltlgegxsgftvhddtankdipvtsvkdaslgqd 60
                                                                                                                                             gialygepwtggtsalpddqlltkgaqkgmgvavfndnlrnaldgnvfdssaqgfatgat
                                                                                                                                                                                                                                                                                                                             dsatgsvtkivpmtasghgvweatvnqnlenwyymyevtgqgstrtavdpyataiapngt
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99.9%;
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Pred. No. 5.6e-284;
0; Mismatches 0;
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Best Local S
Matches 772
                                                                                                                                                                                                                                                                                       The present sequence represents a trimmed enzyme isolated from Bacillus sp. APC-9603. The present specification also describes: (1) a vector containing the DNA encoding a trimmed enzyme; (2) a recombinant microbe transformed by the DNA; and (3) preparation of a trimmed enzyme in which the microbe of (2) is cultured and the trimmed enzyme is collected from the culture. The method can prepare a trimmed enzyme of wide substrate specificity having heat resistance and being active in acid region efficiently.
                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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DB; T97233.
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                                                                                                                               VLVKLSQPLTLGEGXSGETVHDDTANKDIPVTSVKDASLGQDVTAVLAGTFQHIFGGSDW
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Pred. No. 4.9e-272;
3; Mismatches 85;
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Variant bacterial pullulanases
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                                                        N-PSDB; Z89960
                                                                                                                             Bisgard-Frantzen H,
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parent enzyme. The modified enzyme may alternatively or also have an increased activity towards amylopectin and or glycogen compared to the parent enzyme. The enzyme variants are useful for converting starch to one or more sugars. This is useful when starches such as corn, potato, wheat, manioc and rice starch are used as starting materials in commercial large scale production of sugars, such as high fructose syrup, high maltose syrup, maltodextrins, amylose, C4-C6 oligosaccharides and other carbohydrates such as fat replacers. The thermostable debranching enzymes is full taneously before the saccharification step. By debranching using the thermostable debranching enzyme variants during liquefaction together with the action of an alpha-amylase, the formation of panose precursors is reduced, thereby reducing the panose content in the final product and increasing the overall saccharification yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a pullulanase amino acid sequence. Pullulana are debranching enzymes which can attack amylopectin. This sequence represents a parent enzyme from which genetically engineered variant debranching enzymes can be created. The genetically engineered enzyme an improved thermostability at a pH in the range of 4-6 compared to the particular of the parti
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This is the amino acid sequence of pullulanase 6GP3, deduced from an isolated polynucleotide (see v36920) of a Thermotoga maritima clone (5GP3) that grows optimally at 85 degC. The sequence shows 72% amino acid identity to an alpha destrom 6 glucanohydrolase of Caldocellum saccharolyticum. The invention provides 18 polynucleotides (see v36907-24) coding for thermostable glycosidases (see w49858-75) having glucosidase, alpha-galactosidase, beta-mannastable, endoglucanase beta-galactosidase, beta-mannase, endoglucanase or pullulanase activity. Vectors and host cells are also claimed. A method is provided for producing the enzymes by recombinant techniques. A claimed method for generating glucose from soluble
                                                                                                                                                                                                                                                                                                                                                                                        Glycosidase enzymes from organisms of the genera Staphlothermus, Pyrococcus and Thermococcus - for deriving sugar from oligosaccharides, useful in the e.g. food processing, textile or baking industries
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Best Local Similarity 36.3
Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stachyose, verbascose, cellulose, starch, amylose, glycogen, disaccharides, polysaccharides and pullulan) with one of the claimed glycosidases such that glucose is produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell oligosaccharides comprises contacting a sample (selected from dairy products, fruit juice, detergent, textile, guar gum, animal feed, plant biomass or waste product) containing oligosaccharides (selected from maltose, cellobiose, lactose, sucrose, raffinose,
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                          erklqfidv fnyhkgliklrkehpa frlknaeeikkhleflpggrrivafmlkdhaggdp
                                                                                                                                                                                                             SELHAINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSA
                                                                                                                                                                                                                                                                     N-ANGNARIKEFKEMVLSLHREHIGVNMDVVYNHTFAT-QISDFDKIVPEYYYRTMIQVI
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 WGNIIVVYNPNKTVATINLPSGKWAINATSGKVGESTLGQAEGSVQVPGISMMILHQE
                                             SRKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSPENTVAYELTDHVNKDK 896
                                                                                  adkkkewteeelknagklagailltsqgvpflhgggdfcrttnfndnsynapisingfdy
                                                                                                 ND-----SEADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDW
                                                                                                                                        kgfvmggygketkikrgvvgsinydgkliksfaldpeetinyaachdnhtlwdknylaak
                                                                                                                                                                      QGFATGATGLTDAIKNGVEGSIN-----
                                                                                                                                                                                             ralhkidptiilygepwggwgapi----rfgksdvagthvaafndefrdairgsvfnpsv
                                                                                                                                                                                                                                                     dktgaylnesgcgnviaserpmmrkfivdtvtywvkeyhidgfrfdqmglidkktmleve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                edtepyqvvnmeykgngvweavvegdldgvfylyqlenygkirttvdpyskavyannqes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        veliiegykparvimmeild--dyyydg-elgavyspektlfrvwspvskwvkvllfkng
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Pred. No. le-9
38; Mismatches
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RESULT 10
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New thermostable glycosidase(s) - from Thermococcus, Staphylothermus and Pyrococcus, used in the textile, food processing, pharmaceutical, detergent and baking industries
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11-JAN-1996;
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                                                        DNINLTVPAGGAHYTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHT
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39; Mismatches
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                                                             erklq fidv fnyhkgliklrkehpafrlknaeeikkhleflpgarrivafmlkdhaggdp\\
                                                                                                                             adkk kewtee elknaqklagaillt sqgvpflhggqdfcrttnfndnsynapisingfdy\\
                                                                                                                                                             ND-----SEADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDW
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RESULT 11
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(NOVO ) NOVO-NORDISK AS.
                              07-JAN-1998;
                                                            05-JAN-1999;
                                                                                          15-JUL-1999.
                                                                                                                        W09935274-A2
                                                                                                                                                    Fervidobacterium
                                                                                                                                                                                  Fervidobacterium pennavorans; industrial saccharification.
                                                                                                                                                                                                                              Fervidobacterium
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                                                                                                                                                                                                                                                                                                                       Y24380 standard;
                                                                                                                                                                                                                                                            (first entry)
                              9805-0003834
                                                            99WO-IB00069
                                                                                                                                                    pennavorans
                                                                                                                                                                                                                             pennavorans Ven 5 thermostable pullulanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding Fervidobacterium sp. Ven 5 thermostable pullulanase, useful for industrial saccharification processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                              YATAIAPNGTRGMIVDLAKTDPAGWNSDKHITPKNI--EDEVIYEMDVRDFSIDPNSGMK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-430401/36.
DB; X90036.
                                                                                                                                                                                                                                                                                                                                                                                                                     aepikledvnkdvqveiegykparvimmeild--kiyydg-plgfeytpekttirvwspv
                                                                                                                                                                                                                                                                                                                                                                                                                                       GED---PDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DASLGQDVTAVLAGTFQHIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSVCLVLTWAFNVKGQSAHADGNTTTIIVHYFCPAGDYQPWSLWMW----PKDGGGAEYDF 66
DPRNYDVPEGQYATN-ANGNARIKEFKEMVLSLHREHIGVNMDVVYNHTFATQI-SDFDK 593
                                                                                                                                                                                                                                                                      NKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPVFASNSVDETDPTQD---NWGY 535
                                                                                                                                                                                                                                                                                                                                                                sktvdvllyknwddkeptqvvpmkyigngaweavlegnwdgwfykiryfsygeyresvdy 310
                                                                                                                                                                                                                                                                                                                                                                                STQVNVLLYDS-ATGSVTKIVPMTASGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVDP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----eayltgqvdtt--kvgakvtvdgqplklarvekanptdis---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRNALDGNVFDSSAQGFATGATGLTDAIKNGVEGS-----INDFTSSPGETINYVTSHD
                                                                                          qmglmdkvtmlaikselskiepsvvlygepwggwgapi----rfgkadvggtgiaafnde
                                                                                                                      LMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDN 708
                                                                                                                                                                                                  frdalrgsvfnatvkgflmgalaketgvkrgvagsieydevirsfakdpgetinyvevhd\\
                                                                                                                                                                                                                                                         nkalylgltekgtrgpngvttgldhlvelgvthvhllpmfdfwtgdeadkdfersynwgy
                                                                                                                                                                                                                                                                                                               fskavtknsaksaiidfsktnpesw--ekvarpplvapedaiiyeihiadmtgldnsgvk
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Pred. No. 3.5e-88;
46; Mismatches 318; Indels 167;
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P-PSDB;
                                                                                                                                                                                    plasmid pTPI contg. the pullanase gene (Japan Patent Apppln. No. 17437/88) was cleaved by various restriction enzymes and inserted into plasmid pVI18/119. Single-stranded DNA was prepd. using helper phage M13K07 and the base sequence determined by the dideoxy method.
                                                                                                                                                                                                                                        The sequence encoding this protein may plasmid. The heat-resistant pullanase
                                                                                                                                                                                                                                                                        Claim 3; Page 2-3; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1992
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                          Heat-resistant pullulanase gene - and produced in large amts. using
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DB; R23787.
                            nhtlwdknylaaqadttvkwteemlkdaqklagailltsqgipflhagqdfartkkfden\\
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          VTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSDKHITP--KNIEDEVIYEMD
                                                                     dipleig-krylvydhqgavtdlqigavvrtapf------
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                                                                                                                al Similarity
267; Conserv
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Conservative 113;
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                                                                                                                         Score 1228.5;
Pred. No. 8e-
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                                                                                                                 Mismatches
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                                                                                                                                    Length
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n large amts
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RESULT 13
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 Claim 1;
                     A thermostable pullulanase gene recombinant pullulanase free from
                                                        WPI; 1995-100945/14.
N-PSDB; Q85999.
                                                                                     (NISO ) NIPPON SHOKUHIN KAKO
(QPPP ) QP CORP.
(RIKA ) RIKAGAKU KENKYUSHO.
(SHKJ ) SHINGIJUTSU JIGYODAN
                                                                                                                                                                                                                                 Thermus sp
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Fig 2-4; 9pp; Japanese
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Best Local Sim
Matches 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The new thermostable pullulanse gene (Q85999) can be produced recombinant DNA techniques. Esp. the pullulanse prepd. has no
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                                                                                                                                                                                    470 SIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPVFASNSVDETDP-
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                                                                                                                                                                                                                                                                                                                                                                                         230 tnhpdsgavhkgkylglaetntsgpngtatglsyvkelgvthvqlmpfmdfagvderdpq
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                                                                                                                                                                                                                                                                                                                   588 ISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 AYLDASNQVLVKLSQPLTLG-EGXSGFTVHDDTANKDIPVTSVKDASLGQDVTAV--LAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 TFQHIFGGSDWAPDNHSTLLKKYTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINL
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                                                                                                                                                                                                                                          \tt dlmgvhdietmkavrdaldaidpsilvygqgwdlptlfhrnirrrwsnakqlprfayfnd
                                                          AYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGK-WAINATSGKVGESTLGQAEGSVQV
                                                                                            tfwdkmeaanhdepewlrrkrqklataivilaggnpflhsgqefyrtkggdgniyrspda
                                                                                                                                                          TLWDKIALSNPNDSEADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDA
                                                                                                                                                                                                                    NLRNALDGNVFDSSAQGFATGATGLTDAIKNGVEGS---INDFTSSPGETINYVTSHDNY
                                                                                                                                                                                                                                                                 DLMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFND
dgigtwvl
                        PGISMMIL 945
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Best Local Similarity
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                           This sequence represents the Bacillus pullulanase protein. The invention relates to a mutant pullulanase in which at least one methionine residue in the pullulanase is deleted or replaced by an optional amino acid residue other than Cys and Met and/or at least one alanine residue in the amino acid residues constituting pullulanase is deleted or replaced by an optional amino acid residue other than Ala. The mutant pullulanase is useful in bleach-containing detergents. The pullulanase is highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-1997;
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                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                      New mutant pullulanase - useful in bleach-containing
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                                                                                                                        QVG-IIVRTQDWTKDVSADRYIDLSKG--NEVWLVEGNSQIF-------
                                                                                                                                                                      TIIVHYFCPAGDYQPWSLWMW-----PKD----GGGAEYDFNQPADSFGAVASADIPGNPS
                                                                                              nigflvlnttngdkd-ggdkavelfspdlneiwikggsdevflyepvdlpantvrihyer
                        SGFTVHDDTANKDIPVTSVKDASLGQ-.DVTAVLAGTFQHIF--GGSDWAPDNHSTLLKK
                                               tnadyegwglwnwedvespsdgwpngaadaagigkygayyd-----iklk------
                                                                                                                                                                                                                                                                                                                                                                                               13; Page 10-17; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 V62881
                                                                                                                                                                                                                                                                                   to oxidisation.
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edank-1gflfvnkqsggqtgdmtfdmlkqynqlfvkeged---
                                                                                                                                                                                                Conservative 153;
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Pred. No. 2.5
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tes 369;
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27-MAR-1997

(first entry)

Amylopullulanase; alpha-amylase; pullulanase;

detergent additive.

Bacillus alkaline amylopullulanase.

W09255 standard;

Protein; 1938

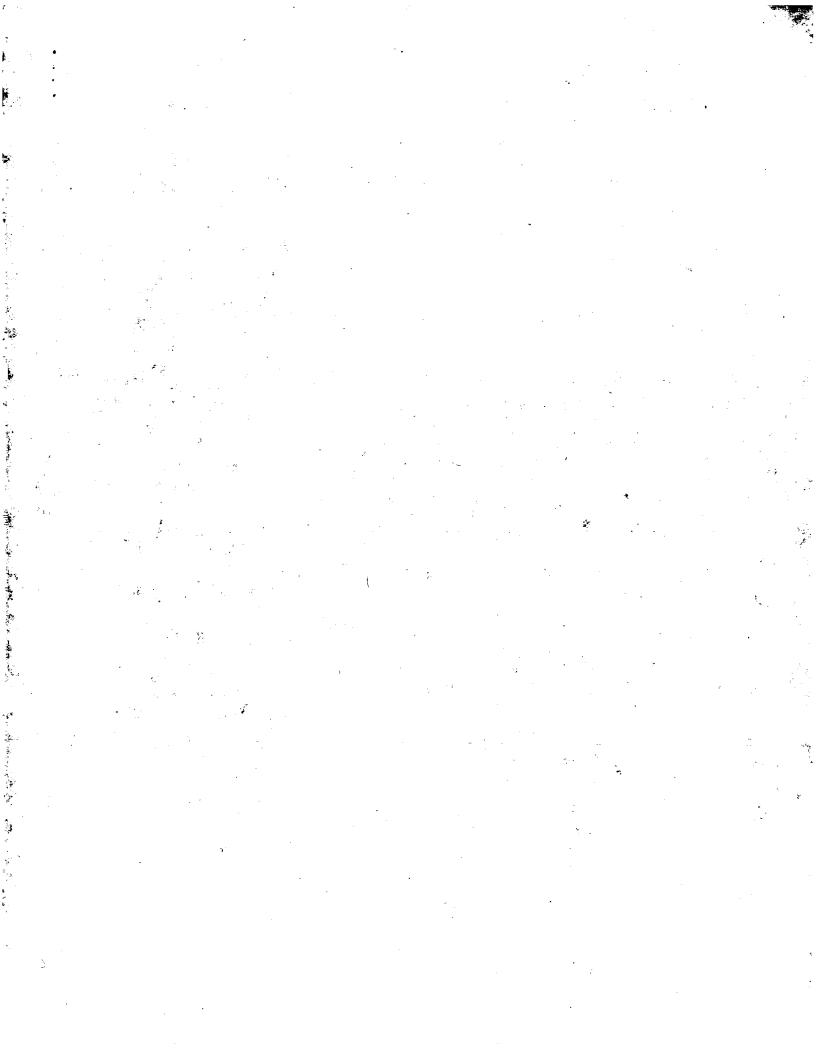
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                                                                                                                                                                                                                                                                                                                 VTSHDNYTLWDKIALSNPNDSEADRIKMD-----ELAQAVVMTSQGVPFMQGGEEMLRXK
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qegtdpgdgdgdgntpppg
                                     ST-----LGQAEGSVQVPG
                                                                       vnadtssrtltlgqdltegvvvvdaeeanvagvaepagfeltaegitleplttvvvrvge 1815
                                                                                                             VN------
                                                                                                                                             trdytaglielrrssdafrlgsrelvdsnvtmvdapeikeqdlvvayrsvstagveyytf 1755
                                                                                                                                                                                 ---YYSGLIHLRLDHPAFRMTTANEINSHLQFLNSPE-----
                                                                                                                                                                                                                     qwrapateapykstymtdadgnpfvypyfihdsydssdiinrfdwekatdaekyp-vnnv 1695
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                                                                                                           -KDKWGNIIVVYNPNKTVATINLPSG----
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Amylopullulanase (W09255) of Bacillus sp. isolate KSM-AP1378 ha. N-terminal alkaline alpha-amylase moiety (see also W09256) and C-terminal alkaline pullulanase moiety (see also W09257). It is the product of an open reading frame in a DNA fraggment (747878) isolated using shotgun cloning and PCR (see also T47879-84).
                                                                 DNA encoding alkaline pullulanase having alkaline alpha-amylase activity - useful for improving the efficacy of dish washing detergents and detergents for clothes, esp. on starch soils
                                                                                                                              Ara
                                                    Disclosure;
                                                                                                      N-PSDB;
                                                                                                                                                              10-MAY-1995;
                                                                                                                                                                             10-MAY-1996;
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US-08-474-345-11
US-08-476-341-11
US-08-961-083-72
US-08-961-083-72
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US-08-476-519-1
PCT-US95-09323-1
US-08-476-519-2
PCT-US95-09323-2
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~~	1. Application 5721127 FORMATION: WI: AMORY, ANT WI: AMORY, ANT WI: ANORY, ANT FINVENTION: P FINVENTION: M FILLIAN CO. CO. CO. CO. CO. CO. CO. CO.	
96. 99. vative	Application US/08474 Application US/08474 T21127 ORMATION: DEWEER, PHILIPPE : AMONTONE PULLULANA INVENTION: PULLULANA INVENTION: PULLULANA INVENTION: PULLULANA INVENTION: PULLULANA SEQUENCES: 15 DENCE ADDRESS: EE: WILLIAN BRINKS H EE: PILICATION STREET PLOPPY disk TYPE: Floppy disk TYPE: Floppy disk R: IBM PC compatible R: FORDY INFORMATION: RSYSTEM: PC-DOS/MS E: PATENTION INMBER: US/08/4 DATE: 07-JUN-195 TCATION UMBER: 37.136 CE/DOCKET NUMBER: 37.136 CE/DOCKET	50000000000000000000000000000000000000
. 8 %	PHILIPPE NTOINE POLLULANAS POUDUCE IT PULLULANAS SS: N BRINKS HO reet, N.W., 15 Compatible PC-DOS/MS- PC-DOS/MS- N Release # DATA: US/08/47 UN-195 35 UMATION: Gadiano, Es Gadiano, Es Gadiano, Es Gadiano, Es Gadiano, Es Gadiano, Es OMBER: 412 FORMATION: 429-0625 3-1850 05 05 11: TICS: acids	0-0-000000000
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RESULT 2
US-08-477-630-11
                                                                Sequence 11, Application Patent No. 5721128 GENERAL INFORMATION:
 APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREI
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILHEM F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 499-0625
TELEPAN: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-630-11
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SOFTWARE: Patentin Reli
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINKS HOFER GILSON
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIC
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 4121-44
TELEPHONE: (202) 429-6625
TELEPHONE: (202) 429-6625
                                                                          TELEFAX: (202) 293-1850
TELEY: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
8-472-293-11
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APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULAN
TITLE OF INVENTION: PULLULAN
TITLE OF INVENTION: PULLULAN
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        GQAEGSVQVPGISMMILHQEVSPDHGKK 956
                                 DQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATGATGLTDAIKNGVEGSINDFT
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Pred. No. 0;
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SEQUENCE CHARACTERISTICS:
LENGTH: 928 amin
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Best Local Similarity
Matches 926; Conserv
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GENERAL INFORMATION:
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TITLE OF INVENTION: PRODUCE TT, PROCESSES FOR THE PRI
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEPAX: (202) 293-1850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET: 2000 K St
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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GVWEATVNQNLENWYYMY EVTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSD
              GVWEATVNQNLENWYYMYEVTGGGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSD
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Patent No. 5
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                                         NAME: Wilhlem F. Gadiano, Esq. REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CCOmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DEWEER, PHILIPPE APPLICANT: AMORY, ANTOINE
                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                STREET: 2000 K St
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
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TELEFAX: (202) 293-1850
TELEX: 650 383-5605
DRMATION FOR SEQ ID NO: 1
                                                                                                                                            APPLICATION NUMBER: US/08/478,341 FILING DATE: 07-JUN-1995
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SEQUENCE CHARACTERISTICS: LENGTH: 928 amino acid

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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
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GQAEGSVQVPGISMMILHQEVSPDHGKK
                              QFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGESTL
                                                         LRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHL
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PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: BE 09300744

FILING DATE: 15-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: BE 09201156

FILING DATE: 28-DEC-1992

ATTORNEY/ACENT INFORMATION:

NAME: Debra J. Glaister, Esq.

REFERENCE/DOCKET NUMBER: 33,888

REFERENCE/DOCKET NUMBER: GC446C1-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (550) 846-7620
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,733
FILING DATE: 23-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,293
FILING DATE: 07-JUN-1995
PRIOR APPLICATION TOWN-1995
                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Genencor
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APPLICATION NUMBER: US 0
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
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APPLICANT: AMORY, ANTOINE
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                  IIVRTQDWTKDVSADRYIDLSKGNEVWLVEGNSQIFYNEKDAEDAAKPAVSNAYLDASNQ 149
I I VRTQDWTKDVSADRY IDLSKGNEVWLVEGNSQIFYNEKDAEDAAKPAVSNAYLDASNQ
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925 Page Mill Road
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APPLICANT: KOSSMANN, Jens
APPLICANT: Emmermann, Michael
APPLICANT: Parelin, Ivar
APPLICANT: Renz, Andreas
TITLE OF INVENTION: DNA MOLECULES CODING FOI
TITLE OF INVENTION: FROM PLANTS
FILE REFERENCE: AGREVO-6
CURRENT APPLICATION NUMBER: US/08/860,339
CURRENT FILING DATE: 1997-11-25
EARLIER APPLICATION NUMBER: DE P4447387.7
EARLIER FILING DATE: 1994-12-22
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SOFTWARE: Patentin Ver
SEQ ID NO 18
LENGTH: 964
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                                                                                                                                                                                                                             RITEFRKMVQALNRIGLRVVLDVVYNHLNSSGPSDDNSVLDKIVPGYYLRR-----DND
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SNWPLIKKRLANPSYKPDKNHIIAAVENFTNLLQIRYSSPLFRLRSAKDIEDRVRFHNNV
                                                                                                                                ------FTSSPGETINYVTSHDNYTLWDKIALSNPNDSEAD-RIKMDEL
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                                                                                                       KQVKGSEVYTYGGTPVGYAMQPIETINYVSAHDNETLFDIVSLKTPTYITVDERCRVNHL
                                                  ATSILALSQGIPFFHAGDELLRSKSLDRDSYNSGDWFNRLDFSYNSNNWGVGLPPKDHNE
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                       ----RKAQYPD-----VFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSP
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Pred. No. 8e-52;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-72
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Best Local Similarity
Matches 149; Conserv
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Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
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NAME: Brookes, A. Anders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                          118
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OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
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                                   YGEPWTGGTSALPDDQLLTKGAQKGM-----GVAVFNDNLRNALDGNVFDSSAQGFATGA 729
                                                                        GGRLGTTHHMTKRLLIDSIKYLVDTYKVDGFRFDMMGDHDAASIEEAYKAARALNPNLIM 177
                                                                                                            EMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIAL 674
                                                                                                                                                   KRIAEFKNLINEIHKRGMGAILDVVYNHT--AKVDLFEDLEPNYYH-FMDADGTPRTSFG
LGEGW----RTYAGDENMPTKAADQDWMKHTDTVAVFSDDIRNNLKSGYPNEGQPAFITGG
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linear
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                                                                                                                                                                                                                                                                                                                         Score 543; DB 4; Length 618; Pred. No. 2.9e-34;
                                                                                                                                                                                                                                                                                                         Mismatches
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Patent No. 5750876
GENERAL INFORMATION:
                                                                                                    Matches 191;
                                                                                                                                Query Match
Best Local
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INFORMATION FOR SEQ
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FILING DATE: 28-ULI-1994
ATTORNEY_AGENT INFORMATION:
NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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                           344 LGNTY--TQKATTFKVWAPTSTQVNVLLYDSATGS--VTKIVPMTASGHGVWEATV-NQN 398
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYPYFIHDSYDSSDAVNKFDWTKATDGKAYPENVKSRDYMKGLIALRQSTDAFRLKSLQD 414
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Pred. No. 1.8e-31;
1; Mismatches 290
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                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
APPLICATION PUBLICATION FILING DATE: 28-JUL-1994
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
             SEQUENCE
                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                    FILING DATE:
CLASSIFICATION:
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                                                                                                                                        APPLICATION NUMBER:
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Containing It and Methods
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                                                                08/281902
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                                                                                                                                    RESULT 11
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Matches
PALENT NO. JUNEANTION:
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
APPLICANT: NO. 5750876e1
                                                                                                Sequence 2, Application US/08476519 Patent No. 5750876
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                                                                                                                                                                                                              RVTD----TATWNEGPNAVALPGSETLI 726
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                                                                                                                                                                                                                                               NATSGKVGESTLGOAEGSVOVPGISMMI 944
                                                                                                                                                                                                                                                                                                                     -----FLNSPEN-TVAYELTDHVNKDKWGNIIVVYNPNKTVATINLP---SGKWAI 916
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         Gene,
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APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
ATTORNEY/ACENT INFORMATION:
NAME: Bonner Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 32,963
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO:
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NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace L. Bonner, Monsanto Company, BB4F
STREET: 700 Chesterfield Parkway No. 5750876th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 777 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US
FILING DATE:
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448
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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CITY: St. Louis
STATE: Missouri
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                      AINPGIALYGEPWT-GGTSALPDDQLLTKGAQKG---MGYAVFNDNLRNALDGNVFDSSA 722
                                                                                               QKFIIDSLKYWVNEYHIDGFRFDLMALLGK----
                                                                                                                                                                                                                                                       -NSVDETDPTQDN-WGYDPRNYDVPECQYATNANGNARIKEFKEMVLSLHREHIGVNMDV 578
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AGGAGADLIAEPWAIGGNS-----
                                                                         QNLIVDSLAYWRDALGVDGFRFDLASVLGNSCQHGCFNFDKNDSGNALNRIVAELPPRPA
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---YQVGGFPAGWAEWNGLYRDALRKKQNKLGV 496
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		531 - NGWITTITOTON-	
	520	Qy 465 DYRDFSIDPNSGMKNKGKYLALTERGT-KGPDNVKTGIDSLKQLGITHVQLMPVFAS Oy 465 DYRDFSIDPNSGMKNKGKYLALTERGT-KGPDNVKTGIDSLKQLGITHVQLMPVFAS	
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		Qy 425 IAPNGTRGMIVDLAKTDPAGWNSDKHITPKNIEDEVIYEM	
	124	OY 399 LENMYRMYEVTG	
	98	39 LGARIDAQANLAFRYISSRATRVEVFLIKNPIGSQEVARLALSKUPAT	
	· w	344	
27;	Gaps	Query Match 10.1%; Score 509; DB 5; Length 777; Best Local Similarity 25.5%; Pred. No. 1.9e-31; Matches 191; Conservative 91; Mismatches 290; Indels 176; G	
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		OGY: II	
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		APPLICATION NUM: FILING DATE: 2	
		FICATION	
		APPLICATION NUMBER	
		PatentIn Release # LICATION DATA:	
		COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS	
		; COMPUTER READABLE FORM: ; MEDIUM TYPE: Flodby disk	
	es	OF INVENTION: Containing It and Methor OF SEQUENCES: 11	
		INVENTION: Novel Isoamylase (
		RESULT 12 PCT-US95-09323-2 ; Sequence 2, Application PC/TUS9509323 ; GENERAL INFORMATION:	
		Db 734 RVTDTATWNEGPNAVALPGSETLI 757	
		OY 917 NATSGKVGESTLGQAEGSVQVPGISMMI 944	
	733	Db 674 PDGAQADSAYFNGADNHALAWRIDGSEFGDSASAIYVAYNGWSGAVDFKLPWPGTGKQWY	
	916	Qy 870FLNSPEN-TVAYELTDHVNKDKWGNIIVYYNPNKTVATINLPSGKWAI	
	673	Db 614 NLDSAANWLYWSRSALEADHETYTKRLIAFRKAHPALRPANFYSASDINGNVMEQLRWFK	
	869	KAQYPDVFNYYSGLIHLRLDHPAFRMTTAN	
	613	Db 554 YGPSDGGEDHNLSWNQGGIVAEQRKAARTGLALLMLSAGVPMITGGDEALRTQFGNNNTY	
	819	EMLRXKGGND	
	553	Db 497 ETVTPGTLATRFAGSNDLYGDDGRKPWHSINFVVAHDGFTLNDLYAYNDKQNNQPWP	
	779	INYVTSHDN	

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RESULT 13
5457037-5
; PATCHT NO. 5457037
; PATCHT NO. 5457037
; APPLICANT: TOGNONI, ANGELO; CARRERA, PAOLO; CAMERINI, BARBARA;
; GALLI, GIUCIANO; LUCCHESE, GIUSEPPE; GRANDI, GUIDO; DI GENNARO, CARLO
; TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE
; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
; NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                Query Match 9.6%; Score 487; DB 6; Length 751; Best Local Similarity 25.6%; Pred. No. 9.7e-30; Matches 184; Conservative 85; Mismatches 271; Indels 180; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/1,797 FILING DATE: 08-JAN-1993 PRIOR APPLICATION DATA:
466 VRDFS-IDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPV----FA 519
                                                                                                              426 A-----PNGTRGMIVDLA---KTDPAGWNSDKHIT-------PKNIEDEVIYEMD 465
                                                                                                                                                                                                        400
                                                                                                                                                                                                                                                                         344 LGNTY--TQKATTFKVWAPTSTQVNVLLYDSATG-SVTKIVPMTASGHGVWEATVNQNL- 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614 NLDSAANWLYWSRSALEADHETYTKRLIAFRKAHPALRPANFYSASDTNGNVMEQLRWFK 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 YGPSDGGEDHNLSWNQGGIVAEQRKAARTGLALLMLSAGVPMITGGDEALRTQFGNNNTY 613
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                                                                                                                                                        68 KAACITGAVYYGYRAWGPNWPYASN-WGKGSQAGFVSDVDANGDRFNPNKLLLDPYAQEV 126
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FILING DATE: 19-AUG-1991
APPLICATION NUMBER: 224,114
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                                                                SQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLVPSTQSTGTKPTRAQKDDVIYEVH 186
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	VH 185	126 SQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLVPSTQSTGTKPTRAQKDDVIYEVH	Вb
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	; EV 125	67 KAAGITGAVYYGYRAWGPNWPYASN-WGKGSQAGFVSDVDANGDRFNPNKLLLDPYAQEV	DЬ
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		: 750	TO.
		FILLING DATE: 13'ANG-1991 APPLICATION NUMBER: 224,114 FILLING DATE: 25-JUL-1988	
		APPLICATION NUMBER: 749,621	
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		TILLE OF INVENTION: CLONING OF THE GENE COLING THE ISOAMYLASE ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME NUMBER OF SECURIARIES. 7	
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	PA 699	640 SGSQLTWYQPSGAVADSNYWNNTSNYAIAYAINGPSLGDSNSIYVAYNGWSSSVTFTLPA	DЪ
,	PS 911	858MTTANEINSHLQFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPS	Qy
	SWY 639	580 QGGDEYLRTLQCNNNAYNLDSSANWLTYSWTTDQSNEYTFAQRLIAFRKAHPALRPSSI	ర్జ
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	KI 770	714 DGNVFDSSAQGFATGATGLTDAIKNGVEGSINDFTSSPGETINYVTSHDNYTLWDKI	Ωу
	466	416 ILREFTVRPAAGGSGLDLFAEPWAIGGNSYQLGGFPQGWSEWNGLFRDSLR	D,
	AL 713	670PGIALYGEPWT-GGTSALPDDQLLTKGAQKGWGVAVENDNLRNAL	Qy
	NR 415	356 LIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYNFDAADSNVAINR	Дb
	N- 669	628 FIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAIN-	Qy
	QN 355	296 YNHTAEGGTWTSSDPTTATIYSWRGLDNTTYYELTSGNQYFYDNTGIGANFNTYNTVAQN	Дb
	QK 627	580 YNHTFATQISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMYQK	Qy
	 VV 295	236 NDVVPNSDANQNYWGYMTENYFSPDRRYANKAAGGPTAEFQAMVQAFHNAGIKVYMDVV	В
	W 579	520 SNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHREHIGVNMDVV	Qy
	DA 235	187 VRGFTEQDTSIPAQYRGTYYGAGLKASYLASLGVTAVEFLPVQETQNDA	D

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RESULT 15
US-09-129-075-4
US-09-129-075-4
Sequence 4, Application US/09129075
Patent No. 6087149
Patent No. 6087149
GENERAL INFORMATION:
APPLICANT: ISUSUMII, No. 60871491ko
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Starch Conversion Pro
FILE REFERENCE: 5262.204-US
CURRENT APPLICATION NUMBER: US/09/129,075
CURRENT FILING DATE: 1998-08-04
EARLIER FILING DATE: 1997-07-02
EARLIER APPLICATION NUMBER: 60/055,867
EARLIER FILING DATE: 1997-08-13
FEARLIER FILING DATE: 1997-08-13
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EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 726
                                                                                                                        Query Match 9.4%; Score 475; DB 3; Length 726; Best Local Similarity 26.8%; Pred. No. 8e-29; Matches 166; Conservative 88; Mismatches 211; Indels 1
                                                                                                                                                                                                                   LENGTH: 726
TYPE: PRT
ORGANISM: Rhodothermus marinus
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                                                    LGATWDGLGVNFALYSOHAEAVELVLFDHPDDPAPSRTIEVTERTGPIWHVYLPGLRPGO 81
                                                                                      LGNTYTQKATTFKVWAPTSTQVNVLLYDSATG-SVTKIVPMTASGHGVWEATVNQNLENW
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                                  VFNYYSGLIHLRLDHPAFR
                                                                      REALKRSLISTLFLSQGVPMLLGGDELSRTQHGNNNAYCQDNEISWYNWQLDTRKQQF-- 573
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Sequence 11423, A	Sequence 9909, Ap	Sequence 11, Appl	Sequence 12462, A	Sequence 32, Appl		Sequence 11850, A	Sequence 186, App	186,	Sequence 9778, Ap	188,	Sequence 188, App	Sequence 12524, A	Sequence 9991, Ap	Sequence 13070, A	Sequence 9428, Ap	Sequence 32, Appl	Sequence 8719, Ap

ALIGNMENTS

Sequence 2, Application US/09262126C GENERAL INFORMATION: APPLICANT: Miller, Brian S. APPLICANT: Shetty, Jayarama K. TITLE OF INVENTION: Modified Forms of Pullulanase FILE REFERENCE: GC396-2 CURRENT APPLICATION NUMBER: US/09/262/126C CURRENT FILING DATE: 1999-03-03 NUMBER OF SED ID NOS: 9 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO SEQ ID NO TYPE: PAT ORGANISM: Bacillus deramificans FEATURE: NAME/KEY: VARIANT LOCATION: (1)...(956) OTHER INFORMATION: Xaa - Any Amino Acid US-09-262-126C-2 US-09-262-126C-2

	Query Match Best Local Matches 95	Query Match 99.9%; Score 5054; DB 5; Length 956; Best Local Similarity 100.0%; Pred. No. 0; Matches 956; Conservative 0; Mismatches 0; Indels 0; Gaps	
Ş	1	MAKKLIYVCLSVCLVLTWAFNVKGQSAHADGNTTTIIVHYFCCPAGDYQPWSLWMWPKDGG 60	
g G	1	MAKKLIYVCLSVCLVLTWAFNVKGQSAHADGNTTTIIVHYFCPAGDYQPWSLWMWPKDGG 60	
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B	61	GAEYDFNQPADSFGAVASADIPGNPSQVGIIVRTQDWTKDVSADRYIDLSKGNEVWLVEG 120	3
्2,	121		3
8	121	NSQIFYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPV 180	0
ΩV	181	- H	0
밁	181	TSVKDASLGQDVTAVLAGTFQHLFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYK 240	0
Q	241	VALNDSWNNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLV 300	0
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δŌ	301		0
В	301	TVTLGEDPDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAP 360	0

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RESULT 2
US-09-262-126C-3
US-09-262-126C-3
: Sequence 3, Application US/09262126C
; GENERAL INFORMATION:
; APPLICANT: Miller, Brian S.
; APPLICANT: Miller, Brian S.
; APPLICANT: Shetty, Jayarama K.
; TITLE OF INVENTION: Modified Forms of Pullula
; FILE REFERENCE: GC396-2
; CURRENT APPLICATION NUMBER: US/09/262,126C
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                          Conservative
                                                                                        20.5%; Score 1039.5;
34.3%; Pred. No. 8.6
tive 125; Mismatches
-QIGAVI-RTAAFDDEFYYDG-ELGAVYTADHT
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nes 272;
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; ORGANISM: Klebsiella
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Thinke 288; Conservative 154; Mismatches
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SEQ ID NO 4
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                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/262,126C
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEO ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Miller, Brian S.
APPLICANT: Shetty, Jayarama K.
TITLE OF INVENTION: Modified Forms of Pullulanase
FILE REFERENCE: GC396-2
                                                                                                                                                                                                                                          LENGTH: 1091
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AVASADIPGNPSQVGIIVRTQDWTKDVS-----ADRYIDLSKGNEVWLVEGNSQIFYNEK 129
                                 VPGEAVTAVENQA--VIHLVDIAGITSSSAADYSSKNLYLWN-----NETCDALS
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Pred. No. 6.5e-48;
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                                IIVVYNPNKTVATINLPSGK-WAINATSGKVGESTLGQ-----AEGSVQVPGISMMIL 945
                                                                                                        YSGLIHLRLDHPAFRMTTANEINSHLQFLNSPENTVAYELTDHVN------KDKWGN 893
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                                                                     YQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSRLDG
                                                                                                                                               RDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAF 956
                                                                                                                                                                                                                       YVSKHDNQTLWDMISYKASQEADLATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFT
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LVVAINAAPESRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADGTVTLPAWSVAVL 1074
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RESULT

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CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 793
TYPE: PRT
ORGANISM: Solanum tuberosum
US-09-463-238-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.4%; Score 528.5; DB 5; Best Local Similarity 26.4%; Pred. No. 5.1e-30; Matches 187; Conservative 100; Mismatches 255;
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APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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                                          RKAQYPDVFNYYSGLI------HLRLDHPAFRMTTANEINSHLQFLNSPE----NTV 878
                                                                                                                                                                                                                PEYYYRTMIQVIIPTDQVLEMK-----LXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLM 650
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KKDESSSDFLRFCGLMTKFRHECESLGLD----GFPTAERLQWHGHTPRTPDWSETSRFV
                                                                                                                                                                                          PNLYQKGGRKPWNSINFYCAHDGFTLADLYTYNNKHNLANGEDNKDGENHNNSWNCGEEG
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                                                                                          EFASIFVKKLRKRQMRNFFLCLMVSQGVPMIYMGDEYGHTKGGNNNTYCHDNYINYFRWD
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                                                                                                                                       -MTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS
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CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR PRIOR HOLD DATE: 1998-07-31
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTMARE: PALENTIN Ver. 2.0
SEQ ID NO 6
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US-09-463-238-6
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APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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FMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSR-KAQYPDVFNYYSGLIHLRLDHPAFRMT 859
                                                                                                                                                                                             NALDGNVFDSSAQG-FATGATGLTDAIKNGVEGSINDFTSSPGETINYVTSHDNYTLWDK 769
                                                                   VSYNNKHNDANGEGGNDGCNDNFSWNCGTEGETSDANTNALRSROMKNFHLALMVSQGTP
                                                                                                                                                  RFIKG---DAGMKGNFATRIAGSADLYR-----VN--KRKPYHSVNFVIAHDGFTLYDL
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; LOCATION: (274, 276)
; OTHER INFORMATION: Xaa - unknown amino
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PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 838
TYPES. TEMP
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APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
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APPLICANT:
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APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regl
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AEAWDCGGLYQVGMFPHWGIWSEWNGKYRDMV---
                                                                                                                                 LMALLGKDTMSKAASELHAINP-GIALYGEPWTGGT-----SALPDDQLLTKGA---
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                                                                                                                                                                                                                                                                          FSPMGRYSSAGLSNCGLGAINEFKYLVKEAHKRGIEVIMDVVFNHTAEGNENGPILSFRG
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                                                                                      LASIL----TRSSSWNAVNVYGNSIDGDVITTGTPLTSPPLIDMISNDPIL-RGVKLI
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                                           -QKGM----GV-AVFNDNLRNALDGNVFDSSAQGFATGATGLTDAIKNGVE 741
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; TYPE: PRT
; ORGANIEM: Solanum tuberosum
US-09-463-238-15
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SEQ ID NO 15
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CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
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APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Edwards, Elizabeth A
APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regl
APPLICANT: Martin, Catherine R
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935 VQVPGISMMILHQEVSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           623 PMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDT------MSKAASELHAINPGIA 673
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Local Similarity 25.5%;
nes 96; Conservative 6
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                                                             SRFLAFMLHD----GNGGDIYLAFNAHHFSIKTAIPSP--PRNRSWYRVVDTNLKSPDDF
                                                                                                                                             GHDTAINNEQWGQLEARKNDHFRFFSKMIKFRLSHNVLRKENFIEKNDITWLEDNWYNEE
                                                                                                                                                                                       NAGDAVNEEDWSR-KAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINS----HLQFLNSP
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; Pred. No. 4.8e-14;
66; Mismatches 142;
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Best Local Similarity 22.4%; Pred. No. 6.9e-12;
Matches 148; Conservative 91; Mismatches 258;
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SEQ ID NO 4
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APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
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CURRENT FILING DATE: 2000-01-21
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TYPE: PRT
ORGANISM: Solanum tuberosum
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                                                    PGETINYVTSHDNYTLWDKIAL-SNPNDSEAD------RIKMDELAQAV
                                                                                                                                                                                                               LMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDN
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             PAFSFNYIARNSGLTLVDLVSFSSNEVASELSWNCGQEGATTNNIVLERRLKQVRNFLFI 676
                                                                                              WNPLTNDSKENLFPHWRRWAEINMRFCDDIRDFLRG-EGLLSNLATRLCGSGDIFAGGRG
                                                                                                                                        ---LRNALDGNVFD-------SSAQGFATGATGLTDAIKNGVEGSINDFTS--S
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                                                                                                                                                                                                                                                                                                       SDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFD 648
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TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR PPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 883
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Sequence 19, Application US/09463238
GENERAL INFORMATION:
APPLICANT: Edwards, Elizabeth A
APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
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; LOCATION: (603, 606)
; OTHER INFORMATION: Xaa - unknown amino
US-09-463-238-19
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Best Local Similarity 22.4%;
Matches 148; Conservative 9
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649 LMALLGKDTMSKAASELHAINÞGIALYGEPWTGGTSALÞDDQLLTKGAQKGMGVAVFNDN |: |: | : |: | : | : | : |
                                                                   476 DNFSYCIKGCQYLN-----IQNALNCNYPIVQQMILDCLRHWVIEFHIDGFVF-
                                                                                             589 SDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFD
                                                                                                                                                              416 GPYFPWHFFSPGNMYGPSGDPLSAIKSMKDMVKKLHANGIEVFLEVVFTHTAEDAPLMNV
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Bustos Guillen, Regla
Martin, Catherine R
Plant Bioscience Limited
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; Sequence 8397, Application US/09739449
; GENERAL INFORMATION:
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RESULT
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 8397
LENGTH: 379
LENGTH: 379
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Length 379; Indels 104;

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; TYPE: PRT
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Best Local :
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APPLICANT: HARKNE
APPLICANT: LOOSMO
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PRIOR FILING DATE: 1996-03-26
PRIOR APPLICATION NUMBER: PCT/CA96/00264
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 10
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PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR FILING DATE: 1995-06-07
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                                    DNVKTGIDSLKQLGITHVQLMPVFASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANG- 553
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EQIQVGADGVK---FAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHLSKDGI
                                                                                                                 AGWN--SDKHITPKNIEDEVIYEMDVRDFSIDPNSGMK-----NKGKYLALTEKGTKGP 494
                                                                                                                                                       ENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGQKNANNQVNTLTLKGE
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KLEIN, Michel H.
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SEQ ID NO 3
LENGTH: 1992
TYPE: PRT
                                                                                   Query Match
Best Local S
Matches 197
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                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/431,718
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR FILING DATE: 1996-03-26
PRIOR APPLICATION NUMBER: PCT/CA96/00264
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                                                                                                                                                                                                                    ORGANISM: Moraxella catarrhalis
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                                        77 ASADIPGNPSQV------GIIVRTQDWTKDVSADRYIDLSKGNEVWLVEGNS 122
AGAGISVTPTEISVDAKSGNVTAPTYNIGVKTTELNSDGTSDKFSVKGSGTNNSLVTAEH 566
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                                                                                     al Similarity
197; Conserv
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LOOSMORE, Sheena M.
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                                                                                     Conservative
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                                                                                 3.9%; Score 196; DB 4;
19.1%; Pred. No. 3.5e-06;
tive 141; Mismatches 377;
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                                                                                                                              Length 1992;
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RESULT 13
US-09-739-449-12578
; Sequence 12578, Application US/09739449
; GENERAL INFORMATION:
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                                                                                                                  1394 NKEQVNDANKKQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLG---EDPDV 310
                                                                                                                                                                                        YVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKL--VAQAQTPDGTLAQMNVKSVI 1393
                                                                                                                                                                                                                            LSNTLANVTNDKGSVRTTEQGNIIKDEDKTRAASIVDVLSAGFNLQGN-----GEAV
                                                                                                                                                                                                                                                                                                                                                                                                                              -----NVFD-----SAQG------FATGATGLTDAIKNG--VEGSINDFTSSPGETI 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGITT-----KVNKGVVRVGIDQTKGLTT----PKLTVGNNNGKG1V1DSQNGQNTITG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAITVGQKNANNQVNTLTLKGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TNTGINAGGKAIT-GLSPTLPSIADQSSR-------NIELGNTIQDKDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LASYLNEVNRTADSALQSFTVKEEDDDDANAITVAKDTTKNAGAVSILKLKGKNGLTVAT 626
                                                                                                                                                                                                                                                                                                --- GNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLR-LDHPAFRMTTANEINSHLQ
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
FITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT APPLICATION NUMBER: US/09/514,000
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 12578
LENGTH: 530
TYDE: PRT
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-12578
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                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                             Sequence 9531, Application US/09739449 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.3%;
Best Local Similarity 20.3%;
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
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                                                                                                                                                                                                                                                                                                                   PPDASQ-----MVMDPNDQ-HTMQLSTLKWTHAETTEGR 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPNDSEADRIKMDEL - - - - - - - - - AQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----PEGTFAAAAEK-----LEYLADVGITTIELMPLATFAGSR-----
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                                                                                                                                                                                                                                                                                                                                                          TDHVNKDKWGNIIVVYNPNKTVATINLPSGKWA-INATSGK 922
                                                                                                                                                                                                                                                                                                                                                                                                    ------FFFFS-----DHPDH--NREQEIRNRLKQAESFQG---
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US-09-739-449-9662
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LENGTH: 532
TYPE: PRT
         APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT FILLING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US.09/514,000
PRIOR APPLICATION NUMBER: US.09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 9662
LENGTH: 533
TYPE: 533
                                                                                                                                                                                                             Sequence 9662, Application US/09739449 GENERAL INFORMATION:
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Best Local Similarity
Matches 115; Conserv
TYPE: PRI
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18.8%; Pred. No. 0.00013;
vative 75; Mismatches 198; Indels 225; Gaps
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; ORGANISM: Agrobacterium tumefaciens US-09-739-449-9662
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                                                                            CLYQGEELGLTEAELAFEDLRDPYGIRFWPAFKGRDGCRTPMVWETGKPNAGFSTAEKPW
                                                                                                                                                                                                                                                                    -AVFNDNLRNALDGNVFD-----SSAQGFATGATGLT------DAIKNGVEGSIND 746
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                                                                                                                 FMQGGEEM------LRXKGG------
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                      FATQISDFDKIVPEYY 599
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Search completed: April 22, 2001, 09:09:21 Job time: 697 sec

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Result
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Maximum
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Maximum Match 100%
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Gapop 10.0 ,
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H84057
G69585
A84112
D75524
A84112
A73760
S11823
T013760
T01376
S731324
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S73084
S7308
S7408
  BVECGX
C83375
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isoamylase (EC 3.2
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glycosyl hydrolase
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probable isoamylas
glycogen operon pr
probable glgX prot
glyX protein (EC 3
                                             glycogen operon pr
probable alpha-glu
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pullulanase amyX -
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243	244.5	245.5	246.5	248	251.5	254	259.5	272	274	278	284	292	320.5	333.5	343.5
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amylase (EC 3.2.1.	1,4-alpha-glucan b	probable 1,4-alpha	neopullulanase (EC	alpha-amylase (EC	cyclomaltodextrina	1,4-alpha-glucan b	1,4-alpha-glucan b	alpha-amylase (EC	hypothetical prote	cyclomaltodextrina	alpha-amylase (EC	pullulanase - Ther	probable maltoolig	amylopullulanase p	alpha-amylase (EC

ALIGNMENTS

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Qy Вb A;Status: preliminary A;Molecule type: DNA A;Residues: 1-843 <ARN> pullulanase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72204 망 Qy 밁 δõ 밁 В Qy Ş Вb Ş A;Cross-references: GB:AE001821; GB:AE000512; NID:g4982421; PIDN:AAD36907.1; PID:g498 A;Experimental source: strain MSB8 . C;Genetics: Nature 399, 323-329, 1999 A;Title: Evidence for lateral gene transfer A;Reference number: A72200; MUID:99287316 A;Accession: H72204 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, A; Gene: TM1845 Query Match Best Local S Matches 349 379 174 199 140 190 259 143 90 91 21 Local Similarity mes 349; Conserv 34 TTIIVHYFCPAGDYQPWSLWMWPKD---GGGAEYDFNQPADSFGAVASADIPGNPSQVGI 90 -KIVPMTASGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDL TVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDDDVSHTLSIQT IVRTQDW-TKDVSADRYIDLSKGN-EVWLVEGNSQIFYNEKDAE------DAAKPAVSNA 142 DGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVT:||: || :| :| | :| : : : TFQHIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINL IVRLNEWQAKDVAKDRFIEIRDGKAEVWILQGVEEIFYEKPDTSPRIFFAQARSNKVIEA 139 EGYKPARVIMMEILD--DYYYDG-ELGAVYSPEKTIFRVWSPVSKWVKVLLFKNGEDTEP Conservative ------DIDVTNY-VRIVLSESL------31.0%; Score 1570; DB 2; 36.6%; Pred. No. 6.9e-82; 145; Mismatches between Archaea andKEEDLRKDVELII 202 291; Length 843; Indels Bacteria Gaps 318 189 259 258 from 22; genome

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pullulanase amyX [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Acccssion: H44057
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodur A;Beference number: A33650; MUID:20263314
A;Accession: H84057
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A; Residues: 1-717 <STO>
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Best Local :
                    456 IEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLM 515
                                                                                                                                                                                    336 QYYYSGDDLGNTYTQKATTFKYWAPTSTQVNVLLYDSATGSVTKIVPMTASGHGVWEATV 395
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                                                                                                                                                                                                                                               Local Similarity
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                                                                                               NQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSDKHITPKN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGLTDAIKNGVEGSIN------DFTSSPGETINYVTSHDNYTLWDKIALSNPND---
                                                                                                                                                  QYVYNG-ELGALYSHERTVFAVWTPVATEVSLLLYENWHTLEAIEYQMKRSPNGVWSVSL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYYNPNKTVATINLPSGKWAINATSGKVGESTLGQAEGSVQVPGISMMILHQE
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                                                                                                                                                                                                                            Conservative 118;
                                                                                                                                                                                                                       21.4%; Score 1084.5; DB 2; 37.5%; Pred. No. 2.8e-54; tive 118; Mismatches 255;
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234 EGNYQYKVALNDSWNNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVES 293

Query Match Best Local Similarity Matches 248; Conserv

Conservative

20.5%; 125;

Score 1039.5; Pred. No. 1e-51 5; Mismatches

272; DB 2;

Indels Length

79;

Gaps

19;

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pullulanase amyX - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: D5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 15-Oct-1999
C;Accession: G69585
C;Accession: G69586
C
A;Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; A;Experimental source: strain 168
                                                                        A; Molecule type: DNA
A; Residues: 1-718 < KUN>
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                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown; translation
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RESULT 4
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alkaline amylopullulanase BH3697 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: A84112
R;Takam1, H; Nakasone, K; Takak1, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans (A;Reference number: A83650; MUID:20263314
A;Accession: A84112
                                                             A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1072 <STO>
A;Cross-references: GB:AP001519; GB:BA0000004; NID:g10176109;
A;Experimental source: strain C-125
C;Genetics:
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A;Gene: BH3697
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                             FLNSPE-----VNKDKWGN
                                                                                   DNSYNAGDAVNEFDWSR----KAQYPD----VFNYYSGLIHLRLDHPAFRMTTANEINSHLQ
                                                                                                                                                                                                                                          MIGEGWRTYVGDEHGGDIMPADQ----DWMQHTESVGVFSDEFRNELKSGFGSEGQPRFIT
                                                                                                                                                                                                                                                                                                    GGGRLGTTHKMSRRILVDSITYWVEEYKVDGFREDMMGDHDAETIQIAYDRAKELNPNIV
                                                                                                                                                                                                                                                                                                                                                              DLGVTHIQLLPVMSYYWGDELANHERELAYSSSGNNYNWGYDPHSYFSLSGMYSENPEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KNIEDEVIYEMDVRDFSIDPNSGMKNK-----GKYLALTEKGTKGPDNVKTGIDSLK 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNLAGYYYHYKIERDGDTKLGLDPYAKSMAAWNNEGSYSIGKAAIVDPSSIGPELDFAEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRG--MIVDLAKTDPAGWNSDKHITP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNTYTQKATTFKVWAPTSTQVNVLLY--DSATGSVTKIVPMTASGHGVWEATVN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKDASLGQDVT-AVLAGTFQHIFGGSDWAPDNHSTLLKK-----VTNNLYQFSGDLPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKGNEVWLVEGNSQIF ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKD---GGGAEYDFNQPADSFGAVASADIPGNPSQVG-IIVRTQDWTKDVSADRYIDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASKVSVLFMIVLLVLSLFTPIMPMHEANADTEADTLRIHYQRSDQQFENLGLWLWGDVRY
LLDIPEISETDLVIGYRATSTDNTGTYYVFVNADTKERTLSLTDDLTEGVVIVDSDEAG-
                                                           HDSYDSSDAINKFDWGKATNKEKYPIHHLTRTYTAGLIELRRSTNAFTHGTLVDVQANVR
                                                                                                                     KRIRLGNTMVLTAQGTAFLHAGQEFGRTKQFRADTGGQAPYKSTYMTDENGKPFVYPYFI
                                                                                                                                       KMDELAQAVVMTSQGVPFMQGGEEMLRXK-----GGN------
                                                                                                                                                                                GGARNIEQIFDNLTAQPHNFTATNPGDVVPYIEAHDNLTLHDVIAQSIRKDPEYHQEEIH
                                                                                                                                                                                                          GATGLTDAIKNGVEGSINDFT-SSPGETINYVTSHDNYTLWDKIALS---NPNDSEADRI 783
                                                                                                                                                                                                                                                                                                                                LEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGFEKREDAIIYEVHVRDFTSDP--GIEEELTAQFGTFASFVDK------LDYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DEKTVILHGSFDAE--LAPYHVTFADKTVVARAGWRLIDALYGYDGELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADLQVESGVKTDLVTVTLGEDPDVSHTLSIQTDGYQAKQVIPRN--VLNSSQYYYSGDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EL---ISLTEMELRETSTIWLSEDDLAEQIHLT-DTNGASVAFDHV-----TIH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NYQYKVALNDS-----W-NNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GDDKTFADLA-------NHPQLFIRQGDDTVYTNPYYQTIEGLVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANPFSDEQTSRYGAYLDVELADDANEI - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NAYLDA-----SNQVLVKLSQPLTLGEGXSGF-TVHDDTANKDIPVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEMKEIWIKEGSDDVFLYEPVDLPDHTVRIHYERSDQSYHHWGLWTWKDVASPSEHWPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSENWPSGGTPFEPEKMTD-YGAYVDIELKENAENIGFLVLNTATGDKD-GNDKHVQLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YNEKDA-----EDAAKPAVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of the radioresistant bacterium Delnococcus radiodurans R1 A;Reference number: A75250; MUID:20036896 A;Accession: D75524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: DR0405
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A; Residues: 1-910 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 260; Conserv
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393 AVNAVKDADAY--NWGYDPYHSMYPEGSYAVNP--AERTKEYROMVMSLNAAGLRYVQDV 448
                                                                                                                                                                                                                        489 KGTKGPDNVKTGIDSLKQLGITHVQLMPVF------
                                                                                                                                                                                                                                                                                                             277 SVFADLSDNSQKPAGWNALKKPALRSFADLSFYELHLRDFSAADASVPAAERGTYLAFTR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 ATGVQTAWAL-----DDLYAYAG-PLGVTWQGNKPTVRLWAPTAQDVK-LHVSRPDGTQ 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 TDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 AGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLS----IQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 SNOVLVKLSOPL-----TLGEGXSGFTVHDDTANKDIPVTSVKDASLGODVTAVLAGTFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               942 MMILH--QEVSPDHGKK 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 KQQQATMLSRDLIVVKPALAQPGAWLTLH------VSPTATLKLGAD------
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                                                                     ASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHREHIGVNMDV 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKIVPMTASGHGVWEATVNQNLENWYYMYEV-----TGQGSTRTAVDPYATAIAPNGTR 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALQAKAPYL-----AGYKL-----LQIRAADRAKLPTALSGQ-LAVSSVLPGGKVLD 164
                                                                                                                                                  PGSDG----MTHLRALAGAGLKAVHLLPTFDIATINEDKGQWQTPGDLTQFGPNSEEQQK 392
                                                                                                                                                                                                                                                                                                                                                                                           GMIVDLAKTD -- PAGWNSDKHITPKNIEDEVIYEMDVRDFS-IDPNSGMKNKGKYLALTE 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERTLPMTRDTQGVWTASGDQSWKGLAYRFEVRVFAPSTGNIETNLVTDPYSVALTRNSTH 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLGFIVHKGD-DKDPGPDGTLTREQGNQLWIVSGNPTPSTTRPDTR-----VRTVGDL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.1%; Score 815.5; DB 2; 26.9%; Pred. No. 9.2e-39; tive 126; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 910;
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	AASGQAERSVLDKIVPO
	Qy 636 WVNEYHIDGFRFDLMALLGKDTNSKAASELHAINPGIALYGEPWTGGTSALP 687
	QY 688 DDQLLTKGAQK730 Comparison
	QY 731GLTDAIKNGVEGSIND
₹	OY 760 SHDNYTLWDKIALSNP-NDSEADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNS 818 M8 :
	OY 819 YNAGDAVNEFDWS
808	OY 845 GLIHLRLDHPAFRMTTANEINSHLQFLNSPENTVAYELTDHVN-KDKWGNIIVVYNPNKT 903
	Qy 904 VATIN 908 : Db 863 AVTLN 867
	RESULT 6 T01688 starch debranching enzyme, pullulanase-type - maize C;Species: Zea mays (maize) C;Date: 19·Feb-1999 *sequence_revision 19·Feb-1999 *text_change 29-Oct-1999 C;Accession: T01688 R;Beatty, M.K.: Rahman, A.: Cao, H.; Woodman, W.; Lee, M.; Myers, A.M.; James, Plant Physiol 119, 255-266, 1999 A;Title: Purification and molecular genetic characterization of ZPU1, a pullul A;Reference number: Z14395; MUID:9907061 A;Accession: T01688 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residuaes: 1-962 GBEA> A;Cross-references: EMBL:AF080567; NID:g3411265; PIDN:AAD11599.1; PID:g3411266 A;Experimental source: endosperm C;Genetics: A;Gene: Zpul C:Function: A;Description: hydrolyzes alpha 1,6 glucosyl linkages
	Query Match 15.8%; Score 797; DB 2; Length 962; Best Local Similarity 27.0%; Pred. No. 1.1e-37; Matches 262; Conservative 143; Mismatches 325; Indels 240; Gaps Qy 134 AAKPAVSNAYLDASNQVLVKLSQPLTLGECXSGFTVHDDTANKDIPVTSVKDASLGQDVT 193 : :-
	OY 194 AVLAGTFQHIFGGSDW-APDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYP 252 :::
	OY 253 SDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGED 307
	Qy 308 PDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNV 367

Gaps

37;

152

334

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alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) - rice
N;Alternate names: pullulanase
C;Species: Oryza sativa (rice)
C;Date: 23-Apr:1999  #sequence_revision 23-Apr:1999  #text_change 21-Jul-2000
C;Accession: T03760
R;Nakamura, Y; Umemoto, T.; Ogata, N.; Kuboki, Y.; Yano, M.; Sasaki, T;
Planta 199, 209-218, 1996
..,...s=rererences: EMBL:D50602; NID:g836661; PIDN:BAA09167.1; A;Experimental source: cv. Fujihikari, endosperm C;Genetics:
                                                                                                 A:Title: Starch debranching A;Reference number: 215063; A;Accession: T03760
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A; Residues: 1-986 <NAK>
A; Cross-references: EMB
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                                                                                                 AQNEKCKMAQLDKNFSYVVTIFNVCPHEVSIEIHDLASLGLELHPIQVNSSDALVRQSAY
                                                                                                                               HVNK-----DK-WGNIIVVYN--PNKT-----VATINLPSGKWAINATSGKVGESTL 928
                                                                                                                                                                 FRPLKNHILSCFDNFVDILKIRYSSPLFRLSTASDIEQRVRFHNTGPSMVPGVIVMSIKD
                                                                                                                                                                                                ----KAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSPEN----TVAYELTD
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                                                                                                                                                                                                                                                                                                                                                                                                 TG-----ATGLTDAIKNGVEGSIND-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQLAKLPPGSDEQQAAIVSIQQEDPYNWGYDPVLWGVPKGSYASNPDGPSRIIEYRQMVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DPTQD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TEKGTKGPDNV-----KTGIDSLKQL---GITHVQLMPVFASNSVDET------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSDEEPNLESFSDISIYELHIRDFSAHDSTVDCNS----RGGFVHLHFRLFRLNLLNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- SDKHITPKNIEDEVIYEMDVRDFS----IDPNSGMKNKGKYLAL-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTASGHGVWEAT
                                                                938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.7%; Score 793; DB 2; 27.6%; Pred. No. 2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NWGYDPRNYDVPEGQYATNANGNARIKEFKEMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277;
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726

609 673 549 621 490

665

746

964

884

904

844 832 784 800 724 565

430 526 370 486 314 446

394 196

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alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) precursor - Klebsiella pneumor N,Alternate names: pullulanase C;Species: Klebsiella pneumoniae C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999 C;Accession: S11823; A32880 R;Kornacker, M.G.; Pugsley, A.P. Mol. Microbiol. 4, 73-85, 1990 Mol. Microbiol. 4, 73-85, 1990 A;Reference number: S11823; MUID:90205629 A;Reference number: S11823; MUID:90205629 A;Status: proliminary a.M.Status: proliminary
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A; Residues: 1-1090 < KOR>
A; Residues: 1-1090 < KOR>
A; Cross-references: EMBL: X52181; NID: g43912; PIDN: CAA36431.1; PID: g43913
R; D'Enfert, C: Pugsley, A.P.
J. Bacteriol. 171, 3673-3679, 1989
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A;Residues: 944-1090 <DEN>
A;Cross-references: GB:M29097; NID:g342046; PIDN:AAA61976.1; PID:g643577
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Klebsiella pneumoniac pulS gene encodes an outer membrane lipoprotein require A;Reference number: A32880; MUID:89291709
A;Reference number: A32880; MUID:89291709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.6%; Score 787.5; DB 2; Best Local Similarity 25.3%; Pred. No. 4.9e-37; Matches 288; Conservative 154; Mismatches 369;
                                                485 PVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQ 544
                                                                                                                                                                                                                                                                369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127
                                                                                                                                                                                                                                                                                                                                                                                              350 QKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTA-SGHGVWEATVNQNLENWYYMYEV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 ESGVKTDLYTVTLGEDPDVSHTLS:QTDGYQAKQVIPRNVLNSSQYYYSGDDL--GNTYT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 F-----TDRYLKLTPTTVSQQVSMRFP----IIL-----SSYAAFKLPDNANVDELLQG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 YOYKVALNDSWNNSYP---SDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNAD--LOV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 VPGEAVTAVENQA--VIHLVDIAGITSSSAADYSSKNLYLWN-----NETCDALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 VKGQSAHADGNTTTIIVHYFCPAG------DYQPWSLWMWPKDGGGAEYDFNQPADSFG 74
                                                                                                                                                     AKMTTHESHTRDLSANDQTVPAELRGKYLAL----TAGDSNMVQHLKTLSASGVTHVELL
                                                                                                                                                                                                                                                                                                                                                           DGGVTFRVWAPTAQQVDVVVY-SADKKVIGSHPMTRDSASGAWSWQGGSDLKGAFYRYAM 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SGCINVIVRDGTDKLIDSDLRVAFGD----FT--DRTVSVIAGNSAVYDSR-- 171
                                                                                        PVFASNSVDE-TDPTQD-----
                                                                                                                                                                                                   EDEVIYEMDVRDFSI-DPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLM 515
                                                                                                                                                                                                                                                           TVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDNLTMPHAQKTKADL
                                                                                                                                                                                                                                                                                              TGQGSTRTAV-----DYYATAIAPNGTRGMIVDL--AKTDPAGWNS----DKHITPKNI 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDVTAVLAGTFQHIFG----GSDWAPDNHSTLL----KKYTNNLYQFSGDLP---EGN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAEDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKDASLG 189
ET-----VAIAAAEDGILISATQVQTAG-----VLDDA-YAEAAEALSYGAQLA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ···--ADAFRAAFGVALAEAHWVDKN--TLLWPGGQDKPIVRLYYSHSSKVAADGEGK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APVA------GPYWVIPLNKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVASADIPGNPSQVGIIVRTQDWTKDVS-----ADRYIDLSKGNEVWLVEGNSQIFYNEK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1090;
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                                                                                                                                                                                                                                                             428
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Query M Best Lo Matches Qy 269 Db 92 Qy 329 Db 141	RESULT 9 T04377 probable all N;Alternate C;Species: C;Date: 23- C;Accession R;Lok, F; submitted t A;Descripti A;Reference A;Accession A;Status: p A;Molecule A;Residues: A;Cross-ref A;Experimen C;Genetics: A;Gene: Hyd, A;Introns: A;Introns: C;Keywords:	Qy 757 Db 836 Qy 816 Db 896 Qy 843 Db 956 Qy 894 Db 1016	Qy 682 Db 718 Qy 730 Db 776	Oy 62 Db 66	Db 545 Qy 574 Db 604
Query Match 15.5%; Score 786.5; DB 2; Length 904; Best Local Similarity 27.9%; Pred. No. 4.1e-37; Matches 233; Conservative 138; Mismatches 277; Indels 187; Gaps 30; 269 FSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLSIQTDGYQAKQVIP 328	RESULT 9 T04377 T04377 T04377 T04377 Probable alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) - barley N;Alternate names: pullulanase C;Species: Hordeum vulgare (barley) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999 C;Accession: T04377 R;Lok, F:, Kristensen, M.; Planchot, V.; Leah, R.; Svendsen, I.; Svenson, B. submitted to the EMBL Data Library, December 1997 A;Description: Isolation and characterization of starch debranching enzyme, limit dex A;Description: T04377 A;Reference number: 215320 A;Accession: T04377 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-904 <lok> A;Cross-references: EMBL:AF022725; NID:92502057; PIDN:AAD04189.1; PID:92677837 A;Experimental source: cv. Igri C;Genetics: A;Gene: HVLD99 A;Introns: 21/3; 70/1; 87/3; 124/1; 169/3; 235/2; 285/2; 305/3; 346/1; 376/2; 407/3; C;Keywords: glycosidase; hydrolase</lok>	7 YVTSHDNYTLWDKIALSNPNDSE-ADRIKMDELAQAVVWTSOGVPFMOGGEEMLRXKGGN 815	82 GTSALPDDOLLTKGAQKGMGVAVFNDNLRNAL-DGNVFDSSAQGFATGA 729	22 RPMVQKEIIDSLKYWVNEYHIDGFREDLMALLGKDTMSKAASELHAINPGIALYGEDWTG 681 	45 DNPQVQALNTLVAQTDSYNWGYDPEHYTVPEGSYATDPEGTTRIKEFRTMIQAI-KQDLG 603 74 VNMDVVYNHTFATQISDFDKIVPEYYYRTMIQVIFTDQVLEMKLXAE 621 11

Query Match 15.2%; Score 771; DB 2; Length 964; Best Local Similarity 26.0%; Pred. No. 3.5e-36; Matches 260; Conservative 133; Mismatches 320; Indels 286; Gaps 39; y 196 LAGTFQHIFGGSDWAPDN	LESULT 10 LESULT 10 LITERATE Spinach LITERATE Spinach LITERATE Spinach LITERATE Spinach LITERATE Spinach LITERATE SPINACH SEQUENCE_revision 01-Sep-1995. #text_change 09-Sep-1997 LITERATE SPINACH LITERATE LITE	428 SGPCGI 642 INGFRE 647 INGFRE 695 GAQ 695 GAQ 695 GAQ 695 TGLTDA 730 TGLTDA 730 TGLTDA 71 IF I I 664 TLFDVI 824 AVNEFD 824 AVNEFD 824 AVNEFD 824 AVNEFD 824 AVNEFD 824 AVNEFD 826 RLDHPA 850 RLDHPA	b 194 GVWSVTGPREWENRYYLYEVDVYHPTKAQVLKCLAGDPYARSLSANGARTWLVDINNETL 253 441 DPAGWNSDKHITPKNIEDEVIYEMDVRDFSI-DPNSGMKNKGKYLALTEKGTKGPDNV 497
RESULT 11 A26879 alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) precursor - Klebsiella pneumon N;Alternate names: pullulan 6-glucanohydrolase; pullulanase C;Species: Klebsiella pneumoniae C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 06-Dec-1996 C;Accession: A26879; S02472 R;Katsuragi, N.; Takizawa, N.; Murooka, Y. J. Bacteriol. 169, 2301-2306, 1987	Qy 789 AQAVWMTSOGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDMS	Qy 423 TAIAPNGTRGMIVDLAKTDPAGGNSDKHITPKNIEDEVIYEMDVRDFS 470 :	Db 70 GSASSVSQSELQGSLNSCRAYWPSKYTFANNYDIGNGSYYLFASKTAALKFTDAGIEGY- 128 Qy 253 SDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDP 308

40 40 A

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A;Title: Entire nucleotide sequence of the pull
A;Reference number: A26879; MUID:87194626
A;Notc: K. aerogenes
A;Accession: A26879
A;Molecule type: DNA
A;Residues: 1-1096 <KAT>
A;Experimental source: strain W70
R;Charalambous, B.M.; Keen, J.N.; McPherson, M.
EMBO J. 7, 2903-2909, 1988
A;Title: Collagen-like sequences stabilize homo
A;Reference number: S02472; MUID:89030658
A;Accession: S02472
A;Status: not compared with conceptual translat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Molecule type: DNA
A:Rosidues: 1-74 <CHA>
A:Rosidues: 1-74 <CHA>
A:Rosidues: 1-74 <CHA>
A:Rosidues: 1-74 <CHA>
A:Roto: past of this sequence was confirmed by protein sequencing C:Genetics:
A:Gene: pulA
A:Gene: pulA
C:Reywords: glycosidase: hydrolase: polysaccharide degradation F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1096/Product: alpha-dextrin endo-1,6-alpha-glucosidase #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
          HIGVN--MDVVYNHTFATQISD----FDKIVPEYYYR-----
                                                                           DSKDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTARIKEFRTMIQAI-KQ
                                                                                                                                                                                                                                          ADLAKMTIHESHIRDLSAWDQTVPAELRGKYLALTAQ----ESNMVQHLKQLSASGVTHI
                                                                                                                                                          ELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLTQLKQN
                                                                                                                                                                                                     QLMPVFASNSVDE-TDPTQD-----
                                                                                                                                                                                                                                                                                   KNIEDEVIYEMDVRDFSI-DPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHV
                                                                                                                                                                                                                                                                                                                              YAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPEGWDGLTMPHAQKTK
                                                                                                                                                                                                                                                                                                                                                                    YEVTGQGSTRTAV-----DPYATAIAPNGTRGMIVDL--AKTDPAGWNS----DKHITP
                                                                                                                                                                                                                                                                                                                                                                                                           --TDSGVTFRVWAPTAQQVELVIY-SADKKVIASHPMTRDSASGAWSWQGGSDLKGAFYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYTOKATTFKVWAPTSTOVNVLLYDSATGSVTKIVPMTA-SGHGVWEATVNONLENWYYM 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVESGVKTDLVTVTLGEDPDVSHT---LSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KVAADS--NGEFSDKYVKLTPTTVNQQVSMRE---PHLASYPAFKLPD-DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLPEGNYQYKVALNDSWNNSYPSDNINLTVPAGGAHVTFSYIPSTH-AVYDTINNPNADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTVSVIAGNSAYYDSRADAFRAAFGVALADAHWV--DKTTLLWPGGENKPIVRLYYSHSS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVTAVLAG-----TFQHIFG----GSDWAPDNHSTLL-----KKVTNNLYQFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKDASLGQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVASADIPGNPSQVGIIVRTQDW----TKDVSADRYIDLSKGNEVWLVEGNSQIFYNEKD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPGEAVQASARQA--VIHLVDIAGITSSTPADYATKNLYLWN-----NETCDALS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LLQGDDGGTAESDGTLSLSHPGADRRRA-GRYLCRRAEALSYGAQL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DWNDVSTTPTGSDKY-----GPYWVI------
                                                                                                     ---NWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHRE
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A:Residues: 1-1038 <JAN>
A:Cross-references: EMBL:L19312
A:Experimental source: ATCC 15050
R:Chapon, C.; Raibaud, O.
J. Bacteriol. 164, 639-645, 1985
J. Bacteriol. 164, 639-645, 1985
A:Title: Structure of two divergent promoters loo A:Reference number: A91807; MUID:86033621
A:Accession: A25025
A;Gene: pulA
C;Keywords: glycosidase; hydrolase; lipoprotein; polysacc
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1038/Product: pullulanase #status experimental <MAT>
                                                                                                                                                                                           R;Kornacker, M.G.; Boyd, A.; Pugsley, A.P. Mol. Microbiol. 3, 497-503, 1989
A;Title: Klebsiella pneumoniae strain K21.
A;Reference number: S04864; MUID:89343636
                                                                                                                                                                                                                                                A; ACCession.
A; Molecule type: DNA
A; Residues: 1-65 <CHA>
A; Residues: 1-65 <CHA>
A; Cross-references: GB: M12503; NID: 9149223;
A; Cross-references: GB: M2503; NID: 9149223;
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A:Title: Regional sequence homologies in starch-degrading
A:Reference number: S38801; MUID:94130317
                                                                                                               A; Molecule type: protein
A; Residues: 'X', 21-31, 'X', 33, 'X'
A; Experimental source: strain K21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Klebsiella pneumoniae
A:Variety: ATCC 15050; strain K21
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994
C:Accession: S38801; A25025; S04864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Janse, B.J.H.; Steyn, A.J.C.; Pretorius, Curr. Genet. 24, 400-407, 1993
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                                                          LNTRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYAMQDNNFN
                                                                                      AD-RIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSR-----
                                                                                                                    LADFILIDKDGAVKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMITYKAAQQAD
                                                                                                                                                  TGATGLTD----AIKNGVE-----GSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSE
                                                                                                                                                                                                                                         GFRFDLMGYHPKAQILSAWDRIKALNPDIYFFGEGWDSNQS--DRFEIASQINLKGTGIG
                                                                                                                                                                                                                                                                                                                                   -FDKIVPEYYYR-----TMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHID
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VGMPRISDDGSNYDVISRVKEMVA: PGEAELKQMTAFYRELTGLRKSSPLFTLGDGSAVM
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25.5%; Pred. No. 2.6e-33;
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                              ---KAQYPDVFNYYSGLIHLRLDHPAFRMTTANEIN
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probable glycogen hydrolase (debranching) - Chlamydia trachomatis (serotype D, C;Species: Chlamydia trachomatis C:Date: 13-Sep-1998 *sequence_revision 13-Sep-1998 *text_change 08-Oct-1999 C;Accession: E71565 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlam A;Reference number: A71570; MUID:99000809
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C;Superfamily: glyX protein
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A; Residues: 1-666 < ARN>
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                DHVNKDKWGNI I VVYNPNKTVAT I NLPSGKWA I NATSGKVGESTLG
                                                                                                                                                                                                                                                                                                                                 --GSTRTA-----VDPYATAI------APNGTRGMIVDLAKTDPAGWNSDKHITPKNI- 456
                                                                                                                                                                                                             VEGSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQ-------
                                                                                                                                                                                                                                                                                         TGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATGATGLTDAIKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -EDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLM 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLSSQKFATDSYIADPYSKNIYSPQLFGSPKQEKDYAFSYLKHEDFDWEGD----TPLHLP
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                                                                                  SRKAQYPDVFNYYSGLIHLRLDHPAFRMTT--ANEINSHLQFLNSP----ENTVAYELT 883
                                                                                                                                                                                                                                                               AGGLYQLGHFPSISTRWSEWNG--CYRDHYKAFLNGDAHQVSS--FASRISGSHDIYPNG
                                                                                                                                                                                                                                                                                                                                                                                                         AGIEVILDVVFNHTGFEGTSCPLPWIDLESYYMVNDHGDLMNFSGCGNTVNTNTPTTLKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVFASNSVDETDPTQD------NWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSLFSSQAQQVTLVLLDPL--SEIHEIPLSSTDHRTGAIWHIEIAGISSEWSYAYKLRGT 83
                                                 DRLAERKELFSFLCQVIALRKAYTELFNTSFLSEDTITWLNTKGSPREWGADHYLAFEL-
                                                                                                                       GETTDPTICALRERQMKNFFLALFLSQGIPMIQSGDEYGHTAYGNNNHWCLDTKINYFLW
                                                                                                                                                        -----AVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDW 830
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Miyajima, da, M.; Yas Synechocys

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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-66 <TET>
A:Gross-references: GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF39177.1; PID:g71903!
A:Experimental source: strain Nigg (MoPn)
C:Gene: TC0312
A:Gene: TC0312
C:Superfamily: glyX protein
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Best Local Similarity
Matches 177; Conserv
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  583 EWTPDHYLAFEL-KHPN---YSLFIAFYSGNERI-ETALPKLRQE-HLAYEKIVDSTTG
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                                                                                            CLDTKINHFLWDRLAERKEFFSFLCQIITLRTTHA -- ELFNTNFLSEETITWLNSQGLPR
                                                                                                                                                                                             SANYSYNFGCEGETTDPNICQLRERQMKNFFLALFLSQGIPMIKSGDEYGHTAYGNNNHW
                                                                                                                                                                                                                                                                                                                       ATGLTDAIKNGVEGSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMD---
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                                               ---PENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGESTLG 929
                                                                                                                                         NAGDAVNEFDWSRKAQYPDVFNYYSGLTHLRLDHPAFRMTTANEINSH-LQFLNS----
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$17009en operon protein (EC 3.2.1.-) glgX-2 - Synechocystis sp. (strain PCC glycogen operon protein slr1857
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: $77094
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Ao, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Gene: 91gx-2
C:Superfamily: 91yx protein
C:Keywords: 91ycosidase; hydrolase
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A; Residues: 1-707 < KAN>
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A;Accession: S77094
A;Status: nucleic acid sequence not shown
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                                                                                         TSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---IPYLQELGVNTIELMPIF---EFDEFEHSRYHPETGEFLVNYWGYSTVNFFAPKAGY 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGK 655
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                                               VSQGVPMLLMGDEMGKTQDGNNNTYCHDSPFNWLNWHLLEQNQAWFRFVKHCIAFRLAHP
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*Klebsiella pneumoniae puls gene encodes an oute lipoprotein required for pullulanase secretion.*

J. Bacteriol. 171:3673-3679(1989).

-i- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYM (1-6)-ALPHA-GLUCOSIDIC LINKAGES-IN PULLULAN FORM MALTOTRIOSE.

-i- SUBGULLULAR LOCATION: ATTACHED TO THE MEMBRA
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Structure of two divergent promoters encoding pullulanase in Klebsiella pne regulated by the malT product.";

J. Bacteriol. 164:639-645(1985).
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                                                                                                                                               SIGNAL
                                                                                                                                                                   Hydrolase;
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SIMILARITY: BELONGS TO FAMILY 13 OF
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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(Rel. 14, Last sequence update)
(Rel. 40, Last annotation update)
PRECURSOR (EC 3.2.1.41) (ALPHA-DEXTRIN
) (PULLULAN 6-GLUCANOHYDROLASE).
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PubMed=2661532;
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N-ACYL DIGLYCERIDE.
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nes 288; Conserv
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LASTSDDQVRHTADLTRIGMAGNIADFYMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVN
                                                       GTSALPDDQLLTKGAQKGMGVAVFNDNLRNAL-DGNVFDS-----SAQGFATGA-----
                                                                                                    RPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIALYGEPWTG
                                                                                                                                                       VN--MDVVYNHTFATQISD----FDKIVPEYYYR-----TMIQVIIPTDQVLEMKLXAE
                                                                                                                                                                                                                                                                                                                                TGQGSTRTAV-----DPYATAIAPNGTRGMIVDL--AKTDPAGWNS-----DKHITPKNI
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                                          NQS--DRFEIASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNE
                                                                                                                                  MNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFA-
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                                                                                       -KLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDS
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                       TGLTDAIKNGVEGSINDF---
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Pred.
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01-AUG-1988
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PULLULANASE
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Klebsiella
 LIPID
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                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentites requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              Katsuragi N., Takizawa N., Murooka Y.;

"Entire nucleotide sequence of the pullulanase gene aerogenes W70.",

J. Bacteriol. 169:2301-2306(1987).

-i- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; I
Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1016
                                                                           Hydrolase;
SIGNAL
                                                                                                 Pfam; PF00128; alpha-amylase; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                      EMBL; M16187; AAA25124.1; ALT_SEQ.
PIR; A26879; A26879.
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-W70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUCOSIDASE) (PULLULAN
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                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                           InterPro;
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SUBCELLULAR LOCATION: ATTACHED
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SIMILARITY: BELONGS TO FAMILY 13 O
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                       FORM MALTOTRIOSE
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(Rel. 08, Last sequence update)
(Rel. 34, Last annotation update)
PRECURSOR (EC 3.2.1.41) (ALPHA-DEXTRIN
)) (PULLULAN 6-GLUCANOHYDROLASE).
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N-ACYL DIGLYCERIDE.
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                                                                                                       TINYVTSHDNYTLWDKIALSNPNDSEAD-RIKMDELAQAVVWTSQGVPFMQGGEEMLRXK
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                           SFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRSSDDGSNYDIIARVKDAVATPGETELKQM
                                                          GGNDNSYNAGDAVNEFDWS-----
                                                                                       VVNYVSKHDNQTLWDMISYKAAQEADLDTRVRMQAVSLATVMLGQGIAFDQQGSELLRSK
                                                                                                                                                 PNELTTLSDDQARHLADLTRLGMAGNLADFVLIDKDGAVKRGSEIDYNGAPGGYAADPTE
                                                                                                                                                                               ----TGLTD------
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                                                                                                                                                                                                                                                                   FA-----KLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEG
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RA Krohn B.M., Barry G.F., Kishore G.M.;
RA Krohn B.M., Barry G.F., Kishore G.M.;
RT "An isoamylase with neutral pH optimum from a Flavobacterium species:
RT Cloning, Characterization and expression of the lam gene.";
RT Cloning, Characterization and expression of the lam gene.";
RT MOL. Gen. Genet. 254:469-478(1997).
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15-DEC-1998 (Rel. 37, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
15-DEC-1998 (Rel. 37, Last annotation
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ISQDPNTATCADGTIYATGAAHRNKDSGLCASKGIALAADATSVGSKPTRALKDEVIYEV
                                          IAPNGTRGMIVD--LAKTDPAGWNSDKHI------
                                                                                     IKNTYGITGAVYYGYRAWGPNWPYDAAWTKGSATGFVSDVDNAGNRFNPNKLLLDPYARE
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                                                                                                                                                                         LGARYDAAQANLAFRVYSSRATRVEVFLYKNPTGSQEVARLALSKDPATQVWSLSLPTST
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"Transcription of the isoamylase gene amyloderamosa SB-15.";
J. Bacteriol. 171:4320-4325(1989).
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PDB; 1BF2; 12-AUG-98.
InterPro; IPR000461; --
Pfam; PF00128; alpha-amylase;
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SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL H
KNOWN AS THE ALPHA-AMYLASE FAMILY. ISOAMYLASE
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VRGFTEQDTSIPAQYRGTYYGAGLKAS
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SGLDLFAEPWAIGGNSYOLGGFPOGWSEWNGLFRDS ->

TVWICLENLGPSAATRTSWYDSRRVYRVEWSVPRQ (IN REF. 1).

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WP -> S (IN REF. 1).

AFRKAHPA -> RSARHLP (IN REF. 1).

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P26501;
           EMBL; M25247; AAA25855.1;
EMBL; A10909; CAA00929.1;
PIR; A37035; A37035.
HSSP; P10342; 1BF2.
                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      "Cloning and nucleotide sequence of the of Pseudomonas sp.";
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                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria.
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Gen. Microbiol. 135:37-45(1989).
CATILYTE ACTIVTY: HYDROLYSIS OF 1.6-ALPHA-D-GLUCOSIDIC LINKAGES IN GLYCOGEN, AMYLOPECTIN AND THEIR BETA-LIMITS I
                                                                                                                                                                                                     INDUCTION: BY MALTOSE SIMILARITY: BELONGS TO
                                                                                                                                                                                     SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, KNOWN AS THE ALPHA-AMYLASE FAMILY. ISOAMYLASE SUBFAMILY.
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DT 01-0CT-1996 0
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85; Mismatches 271
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BY SIMILARITY.
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InterPro; IPR000461; -.
Pfam; PF00128; alpha-amylase;
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GLGX OR RV1564C OR MTCY48.01.
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ACT_SITE 362 362
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                                                                                                                                      QYASTRQAGSAVAEFKTMVRSLHEAGIEVILDVVYNHTAEGNHLGPTINFRGIDNTAYYR
                                                                                                                                                               QYATNANGNARIKEFKEMVLSLHREHIGVNMDVVYNHT----FATQISDFDKIVPEYYYR
                                                                                                                                                                                                                                     H-----PVIIDHLNELNVTAVELMPVHQFLHDSRLLDLGLRNYWGYNTFGFFAPHH
LGKDTMSKAASELHAIN
                                                                                         TMIQVIIPTDQVLEM-----KLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLMAL
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                                               FM--
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SOFT T REPRESENTATION OF SOFT T REPRESENTATION

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P45178;
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01-NOV-1995 (Rel. 32, Last seq
01-NOV-1995 (Rel. 32, Last ann
                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           Science 269:496-512(1995).
-I- FUNCTION: THIS PROTEIN
CATABOLIC OPERON BUT IS
                                                                                                                                                                                                                                                                                      Fine L.D., Fritchman J.L.,
Gnehm C.L., McDonald L.A.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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en the Swiss Institute of Bioinformatics and the EN
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RESULT 9
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Best Local Sim
Matches 176;
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InterPro; IPR000461; ...
( PFam; PP00128; alpha-amylase; 1.
Glycogen blosynthesis; Hydrolase; Glycosidase.
A GLYCOgen blosynthesis; Hydrolase; Glycosidase.
T ACT_SITE 333 333 BY SIMILARITY.
ACT_SITE 440 440 BY SIMILARITY.
ACT_SITE 440 440 BY SIMILARITY.
CSQ AA; 75290 MW; E2B71F610E8BICAC
GLGX_ECOLI PRT; 6
P15067; P76693;
01-APR-1990 (Rel. 14, Created)
01-NOV-1995 (Rel. 32, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
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                                                                                                                                                                                                                                                                                    AQY-PDVFNYYSGLIHLRLDHPAFRMTTANE----INSHLQFLN------SPENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLAVTGVKTGTEYAFRIHGEFANPQKLILDPYAKAV--NGK----PDLSSEESRSWFLLS
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24.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- DGNVFDSSAQGFATGATGLTDAIKNGVEGSINDFT
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2B71F610E8B1CAC
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                   update)
                                                                 657
       update)
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2e-15;
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Best Local (
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ACT_SITE
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J01616; AAA98735.1; AI
EMBL; J18997; AAA58229.1; --
EMBL; AE000419; AAAC76456.1;
PIR; JT0400; BVECGX.
HSSP; P10342; 1BF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Analysis of the Escherichia coli glycogen gene cluster suggests catabolic enzymes are encoded among the biosynthetic genes.*; Gene 70:363-376(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOGEN OPERON PROTEIN GLGX OR GLYX.
                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                Pfam;
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  182
                               494
                                                                                        453
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                                                                                                                    89
                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: THIS PROTEIN MAY BE PART OF A GLYCOGEN BIOSYNTHETIC/
CATABOLIC OPERON BUT IS NOT REQUIRED FOR GLYCOGEN SYNTHESIS.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A STOP
CODON IN POSITION 507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome sequence of nce 277:1453-1474(1997).
                                                                                                                 LRYGYRVHGPWQPAEGHRFNPAKLLIDPCARQIDGEFKDNPLLHAGHNEP-DYRDNAAIA
                                                                                                                                            WYYMYEVTGQ-----GSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSDKHIT 452
                          PDNVKTGIDSLKQLGITHVQLMPV--FASNSVDETDPTQDNWGYDPRNYDVPEGQYATNA
                                                          PKCVVVVDHYDWEDDAPPRTPWGSTIIYEAHVKGLTYLHPEIPVEIRGTYKALGH-----
                                                                                        PKNI -----EDE---
                                                                                                                                                                         LGAHYDGQGVNFTLFSAHAERVELCVFD-ANGQEHR---YDLPGHSGDIWHGYLPDARPG
                                                                                                                                                                                                                                   160;
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                                                                                                                                                                                                                                 Similarity 23.4
60; Conservative
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E 336 336
E 443 443
-PVMINYLKQLGITALELLPVAQFASEPRLQRMGLSNYWGYNPVAMFALHPAYA--C
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73576
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36 BY SIMILARITY.
43 BY SIMILARITY.
48 BY -> YY (IN REF. 2).
73576 MW; AA9EFC1F67FD0420 C
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                                                                                                                                                                                                                                96;
                                                                                   ---VIYEMDVRDFS-IDPNSGMKNKGKYLALTEKGTKG
                                                                                                                                                                                                                                                Score 363;
Pred. No.
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    RESULT 10
APU_THETY
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P16950;
01-AUG-1990 (Rel. 15, 0
01-AUG-1990 (Rel. 15, 1
15-JUL-1999 (Rel. 38, 1
                                                                                                                                                                                              Melasniemi H., Paloheimo M., Hemioe L.;
"Nucleotide sequence of the alpha-amylase-pullulanase Clostridium thermohydrosulfuricum.";
J. Gen. Microbiol. 136:447-454(1990).
                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOPULJULANASE PRECURSOR (ALPHA-AMYLASE/PULLULANASE) [INCLUDES:
ALPHA-AMYLASE (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE);
PULLULANASE (EC 3.2.1.41) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)
(ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
                                                                                                                                                         SEQUENCE OF 32-39.
STRAIN-E101-69;
                                                                                                                                                                                                                                                                      STRAIN-E101-69
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                             FIBRONECTIN TYPE III MEDLINE=93028390; Put Bork P., Doolittle R.
                                                                                    Biochem.
                                                                                                pullulanase
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1516;
                                                                                                                                                                                                                                                                                                                            Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                           thermohydrosulfuricum)
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter thermohydrosulfurious (Clostridium
                                                                                                                              Melasniemi H.;
                                                                                                                                           MEDLINE-88268757;
                                                                                                                                                                                                                                                    MEDLINE-90362027;
                                                                                                             Purification and some
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             Proposed
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                          93028390; PubMed-1409594; Doolittle R.F.;
acquisition of an animal protein domain l. Acad. Sci. U.S.A. 89:8990-8994(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DTMSKAASELHAINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVF---
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                                                                                  on and some properties of produced by Clostridium 250:813-818(1988).
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                                                                                                                                         PubMed=3260488;
                                                                                                                                                                                                                                                         PubMed=2391488;
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                                                                                                             extracellular alpha-amylase-
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SIMILARITY: BELONGS TO FAMILY 13 OF
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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LALTEKGTKGPD------NVKTGIDSLKQLGITHVQLMPVFASNSVDETDPTQDNWGYD
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Ol-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOPULIULANASE PRECURSOR (ALPHA-AMYLASE/PULLULANASE) (INCLUDES:
ALPHA-AMYLASE (EC 3.2.1.1) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE);
PULLULANASE (EC 3.2.1.4) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)
QALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
Unpublished observations (NOV-1994).

-I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

-I- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO FORM MALTOTRIOSE.
                                                                                                                                                                                                                                                                                                                           Thermoanaerobacter saccharolyticum.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Thermoanaerobacter group; Thermoanaerobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROI KNOWN AS THE ALPHA-AMYLASE FAMILY.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DO CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN BY AN EXTRA C-TERMINAL SEGMENT OF 9 RESIDUES THAT SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM A PUC-TYPE VECTOR.
<u>۾</u>
                                                                                                                                                                                                                                                                                                                         RYIDLSKGNEVWLVEGNSQIFYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGX
                                                                                            VPMTASG---
                                                                                                                                YQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKI
: | |:: | ||: | |:
                                                                                                                                                               NIWTNYSPTLTGLDNNIYYDDLKHDTHD----PFFRNPFGAIKVGQ----TVTLRIQAKN
                                                                                                                                                                                         ٨V
                                                                                                                                                                                                             NNLYQFSGDLPEGNYQYKVALNDSWNNSYPSD-----NINLTVPAGGAHVTFSYIPSTH
                                            MIVDLAKTDPAGWNSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTK
                                                                   LPMTRIGESPDGNYEYWEIKLSFDHPTRIWYYFILKDG---TKTAY--YGDNDDQLGGLG
                                                                                                                     HD-----
                                                                                                                                                                                                                                                                                  SGFTVHDDTANKDIPVTSVKDASLGQDVTAVLAGTFQHIFG-GSDWAPDNHST-LLKKVT
                                                                                                                                                                                                                                                                                                                                                       ----DSNITIMQYVGNGLYEFTTPTQLKAGSYQYKVALNHSWNGGGVPSQGNLTLNLTND
                                                                                                                                                                                                                                                                                                                                                                             MWPKDG------GGAEYDFNQPADSFGAVASADIPGNPSQVGIIVRTQ-DWTKDVSAD
                                                                                                                                                                                                                                                                                                                                                                                                      KKFISFVMSLLLVLTAAFSSMPFHNVYAADNASVVANIV-----GDFQDQLGDSNWNI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00128; alpha_amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L07762; AAA19800.1;
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                                                                                           ---HGVWE--ATVNQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRG
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                                                                                                                    ·LESARISY-WDDINKTRTE----
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                      -----FELTVYDKNFDTNDWMKGAVMYQIFPDRFYN
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ANYLOPULLULANASE.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.
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Pred. No. 1e-10;
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                                                                                                                                                                                                                                                            ------LVGTIQSAIGAGKDWDPGTSTAIMIDDNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF GLYCOSYL HYDROLASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal;
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BY THE PRESENCE (
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RESULT 1:
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P38939;
01-FEB-1995
01-FEB-1995
15-JUL-1999
                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOPULLULANASE PRECURSOR (ALPHA-AMYLASE/PULLULANASE) [INCLUDES:
ALPHA-AMYLASE (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)
PULLULANASE (EC 3.2.1.41) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)
                                                                                                                                                                                                                                                          Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum) Bacteria; Firmicutes; Bacillus/Clostridium group; Thermoanaerobacter group; Thermoanaerobacter.
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                              NCBI_TaxID-1757;
                                                                                                                                                                                                                                                                                                                   (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
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(1-6)-ALPHA-GLUCOSIDIC LINKAGES IN EFORM MALTOTRIOSE.
SUBUNIT: MONOMER.
SIMILARITY: BELONGS TO FAMILY 13 OF
KNOWN AS THE ALPHA-AMYLASE FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLRDGVAFKDLINGDKSYTINGGQITINIPAMSGVMLISDDGQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDSLKQLGITHVQLMPVFASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQVLKTGDLETLYAQNDVYAIGRRIINGKDAFGNSYPDSAAIVAINRSNSDQQITIDTTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                GNYQYKVALNDSWNNSY-----PSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNA-
                                                                                                                                                                                                                                                                                                                                                                                                       DIPVTSVKDASIGQDVTAVLAGTFQHIFG-GSDWAPDNHSTLLKKVT-NNLYQFSGDLPE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADSFGAVASADIPGN-PSQVGIIVRTQDWTKDVSADRYIDLSKGN-----EVWLVEGN 121
VYNHTFATQI - - -
                                                                                                                                                      DPAGWNSDKHI-TPKNIEDEVIYEM---
                                                                                                                                                                              SPDGQYEYWEVKLSFDYPTRIWYYFILKDG---TKTAY--YGDNDEQLGGVGKATDTVNK
                                                                                                                                                                                                                                   NHDLESAKISY-WDDIKKTRTE--
                                                                                                                                                                                                                                                                                    PDNNIYYDDLKHDTHDPFFRFAFGAIKTGDTVTLRI------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AETDTAPAIANVVGDFQSKIG----DSDW--NINSDKTVMTYKGNGFYEFTTPVALPAGD
                         ----NHRYDTTDY---
                                                  TDPTQDNWGYDPRNYDVPEGQYATNANGNARIKE-----
                                                                                                  -NSGMKNKGKYLALTEKGTKGPD---
                                                                                                                            DFELTVYDKNLDTPDWMKGAVMYQIFPDRFYNGDPLNDRLKEYSRGFDPVEYHDDWYDLP
                                                                                                                                                                                                                                                         RNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTASG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            YEYKVALNHSWEGGGVPSQGNLSLHLDSDSVV-----TFYYNYNTSSVTDSTKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001777; -
                                                                                                                                                                                                       HGVWEATVNQNLEN--WYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKT
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628
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                                                                                                                                                                                                                                                                                                            DLQVES-----GVKT-DLVTVTLGEDPDVSHTLSIQTDGYQAKQVIP
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                                                                          TGDGIWNNDFFGGDLQGINDKLDYLKNLGISVIYLNPIFQSPS---
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20.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156;
                         -----TKIDELLGDLDTFKTLMKEAHARGIKVILDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
MW; CB2635960539CAlD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMYLOPULLULANASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 333.5; DB 1;
Pred. No. 1.3e-10;
6; Mismatches 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                  ----NVKTGIDSLKQLGITHVQLMPVFASNSVDE
                                                                                                                                                     ----DVRDFS--IDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage by
                                                FKEMVLSLHREHIGVNMDV
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                                                                                                                                                                                                                                                                                    -QAK----
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RESULT 13
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X MEDLINE-94252998; PubMed-8195085;
XA Matuschek M., Burchhardt G., Sahm K., Bahl H.;
YA Matuschek M., Burchhardt G., Sahm K., Bahl H.;
IT "Pullulanase of Thermoanaerobacterium thermosulfurigenes EM1
T (Clostridium thermosulfurogenes): molecular analysis of the gene,
T composite structure of the enzyme, and a common model for its
T composite structure of the enzyme, and a common model for its
T attachment to the cell surface.";
I Bacteriol 176:3295-3302(1994)

C 1- CATALYTIC ACTIVITY: ENDOMORDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
C LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -1- CATALYTIC ACTIVITY: STARCH DEBRANCHING ENZYME, HYDROLYZES
CC -1- CATALYTIC ACTIVITY: STARCH DEBRANCHING ENZYME, HYDROLYZES
CC -1- CATALYTIC ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOPULLULANASE PRECURSOR (ALPHA-AMYLASE/PULLULANASE) (PULLULANASE TYPE II) [INCLUDES: ALPHA-AWYLASE (EC 3.2.1.1) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE); PULLULANASE (EC 3.2.1.41) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
                         This
       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thermosulfurogenes).
Bacteria; Firmicutes; Bacillus/Clostridium group;
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P38536;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                              KNOWN AS THE ALPHA-AMYLASE FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAII SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                              PTM: GLYCOSYLATED.
SIMILARITY: BELONGS TO FAMILY 13
                                                                                                                                                      SUBCELLULAR LOCATION:
S-LAYER ANCHOR.
                                                                                                                                                                                           FORM MALTOTRIOSE
SWISS-PROT entry is copyright. It is produced through a collaboration -
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Best Local
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SEQUENCE
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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InterPro; IPR001119;
InterPro; IPR001777;
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                              VMMDVVYNHTEATQISDEDKIVPEYY-----YRTMIQVIIP---
   IILDGVFNHT
                                                                                                                                                                                                                              WNSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKG---
                                                                                                                                                                                                                                                                                                                                                                                                                             TYTOK - - -
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                                                                                            LMPVFASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHREHIG
                                                                                                                              RGNDPIEFHNNWNDLPDNPNNAGTPGYTGDGIWSNDFFGDLKGIDDKLDYLKGLGVSVIY
                                                                                                                                                                                                                                                            NFEYWEIKLSFDHPTRIWYYFILKDG~~~TKTAY~~YGDNDDQLGGVGKATDTVNKD~~~
                                                                                                                                                                                                                                                                                            --- VWE-- ATVNONLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAG
                                                                                                                                                                                                                                                                                                                            DTHDSFFRNPFGAVKVDQTVTLRIQAKNHDLESARISYWDDINKIRIELPMTRIGESPDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYQYKVALNHSWDGGGVPSQGNLTLNLANDSYVTFWFDYNTQSVTDSTKYTPIANDKLPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osidase; Carbohydrate metabolism; enzyme; Glycoprotein.
                                                                                                                                                                                              -----FELTVYDKNFDTPDWMKGAVMYQIFPDRFYNGDTSNDHAKTLS
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DSIYFNRYGKYPGLGAYQAWKEGNQSLSPYGDWYTINSDGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123;
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BY SIMILARITY.
BY SIMILARITY.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
SIH 1.
SIH 2.
SIH 3.
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Pred. No. 3.4e-08;
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06C23070E453B574 CRC64;
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CYCLOMALTODEXTRINASE (EC 3.2.1.54) (CDASE) (C
                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         Oguma T., Matsuyama A., Kikuchi M., Nakano E.;
"Cloning and sequence analysis of the cyclomaltodextrinase gene
Bacillus sphaericus and expression in Escherichia coli cells.";
Appl. Microbiol. Biotechnol. 39:197-203(1993).

-i- FUNCTION: HYDROLYZES CYCLODEXTRINS. CAN ALSO ACT ON INEAR
MALTODEXTRINS, MITH THE EXCEPTION OF MALTOSE. THE PH OPTIMUM
PH 8.0 AND THE OPTIMAL TEMPERATURE IS 45 DEGREES C.

-i- CATALYTIC ACTIVITY: CYCLOMALTODEXTRIN + H(2)0 - LINEAR
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NCBI_TaxID=1421;
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Bacteria; Firmicutes; Bacillus/Clostridium
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STRAIN=E-244;
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                    EMBL;
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SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY. CDASE MOST CLOSELY RESEMBLES NEOPULLULANASE FROM B. STEAROTHERMOPHILUS AND ALPHA-AMYLASE-PULLULANASE FROM C.THERMOHYDROSULFURICUM.
                                                                                                                                                                                                                                                                                             SUBUNIT: MONOMER.
                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                    x62576;
                  CAA44454.1;
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Hydrolase; Glycosidase.
ACT_SITE 327 327 BY
ACT_SITE 356 356 BY
ACT_SITE 423 423 BY
SEQUENCE 591 AA; 67899 MW;
                                                                                                                                                                                                                         CDAS_THEET P29964;
                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
CYCLOMALTODEXTRINASE (EC 3.2.1.54) (CDASE) (CYCLOMALTODEXTRINASE HYDROLASE, DECYCLING).
        MEDLINE-92355516; PubMed-1644767
Podkovyrov S.M., Zeikus J.G.;
Podkovyrov S.M., Zeikus J.G.;
Structure of the gene encoding
                                                                                                                           Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum). Bacteria; Firmicutes; Bacillus/Clostridium group;
  thermohydrosulfuricum
                                                                     SEQUENCE FROM
                                                                                               Thermoanaerobacter NCBI_TaxID=1757;
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                                          PubMed=1644767;
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CONFLICT
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"Analysis of the catalytic center of cyclomaltodextrinase from Thermoanaerobacter ethanolicus 39E.";
FEBS Lett. 317:259-262(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGEN
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J. Bacteriol. 174:5400-5405(1992).
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SUBUNIT: MONOMER.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY. CDASE MOST CLOSELY RESEMBLES NEOPULLULANASE FROM B. STEAROTHERMOPHILUS AND ALPHA-AMYLASE-PULLULANASE FROM C.THERMOHYDROSULFURICUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: HYDROLYZES CYCLODEXTRINS, CAN ALSO ACT ON LINEAR MALTODEXTRINS, WITH THE EXCEPTION OF MALTOSE.

CATALYTIC ACTIVITY: CYCLOMALTODEXTRIN + H(2)O - LINEAR
                                            LPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATGA---TGLTDATKNGVEG
                                                                                                                                                                                                                                                                                                                            DETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHREHIGVNMDVVYNHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIKPMVLTHINELFDYYETTLELNKKFVYFFYLVSDGGEKL-----YYTE------
LRGDQF-------DSVMNYPFRNA----VVDFFAKRKISASRFNTMITEQLMRHMD-
                                                                                             QKYLLEVAEYWIKEVDIDGWRLDVANEIDHHFWRKFREVVKAAKPEAIIVGEVWHDASPW
                                                                                                                                      QKFIIDSLKYWVNEYHIDGFREDLMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSA 685
                                                                                                                                                                                       GYDFFAFQ--DVIKNGKKSKYWDWFNIYEWPIKTHGKPSYEAFADTVWRMPKLMTKNPEV
                                                                                                                                                                                                                                        ----FATQISDFDKIVPEYYYRTMIQVI---IPT------DQVLEM-KLXAERPMV
                                                                                                                                                                                                                                                                                  HKYD-TTDYYTIDPHFGDT------QKARELVQKCHDNGIKVIFDAVFNHC
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E->Q: LOSS OF ACTIVITY.
D->N: LOSS OF ACTIVITY.
E -> G (IN AA SEQUENCE).
E -> G TEN A SEQUENCE).
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Pred. No. 1e-06;
4; Mismatches 212;
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                                                                AFRMTTANEINSHLOF-----LNSPENTVAYELTDHVNKDKWGNIIVVYN--PNKTVATI 907
                                                                                         YYGDEV-
                                                                                                                                    SVNRV-----MENLIGSHDTERF---LTLAN-----GMVARMKLALVFQFTFVGIPYI
                     NLPSGK
                                          913
                                                                                        -GMVGDYDPDCRRCMIWEEEKQNKSIFNFYKKLISIRRE--
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Search completed: April 22, Job time: 352 sec 2001, 09:11:53

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Minimum
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Listing first 45 summaries
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O9xdb5 fervidobact P71095 bacteroides 059319 caldocellum 069008 thermus sp. O9k7u5 bacillus ha 034587 bacillus ha 034587 bacillus ha 034587 bacillus ha P70983 bacillus sp. O9k6n1 bacillus sp. O9xxb0 deinococcus O64454 oryyaa sativ 081638 zea mays (m. P93416 oryyaa sativ 099758 hordeum vul 048541 hordeum vul 048541 hordeum vul 048541 hordeum vul 048541 hordeum vul 041386 spinacia ol 084046 chlamydia t Q9rm63 myroides od 09pkz6 chlamydia m
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Q9p9a0

ALIGNMENTS

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	125 FYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVK 184	Qy
	66	DЬ
	67 NQPADSFGAVASADIPGNPSQVGIIVRTQDW-TKDVSADRYIDLSKGN-EVWLVEGNSQI 124	Qy
		Дb
	10 LSVCLVLTWAFNVKGQSAHADGNTTTIIVHYFCPAGDYQPWSLWWWPKDGGGAEYDF 66	δõ
28;	Query Match 28.2%; Score 1428.5; DB 2; Length 849; Best Local Similarity 34.9%; Pred. No. 2e-78; Matches 339; Conservative 146; Mismatches 318; Indels 167; Gaps	
	SEQUENCE 849 AA; 96591 MW; 1CB6B2A882A351A2 CRC64;	SQS
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01-FEB-1997
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        SEQUENCE FROM N.A.
                                 Bacteroides thetaiotaomicron Bacteria; CFB group; Bactero NCBL_TaxID=818;
STRAIN-5482;
                                                                                       PULLULANASE.
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                                                                                                                                                                                                                                                                  VAFVLKD--EKDPWKEILVIYNGDTKDQQFTLPDGTWNVVVDKDNAGTKVLYQVSGKINI
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RESULT Q59319
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Best Local S
Matches 266
                                                                           Q59319 PRELIMINARY; PRT; 825 AA.
Q59319;
Q1-NOV-1996 (TrEMBLrel. Q1, Created)
Q1-NOV-1996 (TrEMBLrel. Q1, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. J3, Last annotation update)
ALPHA-DEXTRIN 6-GLUCANOHYDROLASE (EC 3.2.1.41)
(ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE) (PULLULANASE)
(PULLULAN 6-GLUCANOHYDROLASE) (LIMIT DEXTRINASE) (DEBRANCHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97113539; PubMed-8955399; D'Elia J.N., Salyers A.A.; Contribution of a neopullulanase, a glucosidase to growth of Bacteroides J. Bacteriol. 178:7173-7179(1996). EMBL; U67061; AAC44685.1; -.
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  saccharolyticum
                                                            6-GLUCANOHYDROLASE)
  (Caldicellulosiruptor
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Eur. J. Biochem. 0:0-0(0).
-!- CATALYTIC ACTIVITY: STARCH
ALPHA-GLUCOSIDIC LINKAGES
MALTOTRIOSE.
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PFAM; PF00128; alpha-amylase;
Hydrolase; Glycosidase,
SEQUENCE 825 AA; 95732 Mw;
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                                                                                    KEKKILQLPEGSWYVKANDGIVFPDSFEKEAIGSFEIAPVSLFIAYQK
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ
EMBL; AF060205; AAC15073.1; -
INTERPRO; IPR000461; -
PFAM; PF00128; alpha-amylase; 1.
SEQUENCE 718 AA; 80446 MW; 8F7C0D22405EA8
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Bacteria; Thermus/Deinococcus
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01-OCT-2000
01-OCT-2000
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; APO01518; BAB06983.1;
SEQUENCE 717 AA; 81865 MW; 2A979DFA25638920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group:
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9K7U5;
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697 FNCHTVSVQSRSSMVLYR
                           931 AEG-SVQVPGISMMILHQ
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                                                                                                             HGEGNSYNSPDWINQLDWSRRAIYAADVEYVKGLIALRKAHRAFCFSTFSEVNTHWCPLK
                                                                                                                                 GGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHPAFRWTTANEINSHLQFLN
                                                                                                                                                                                                                                                              KGAOKGMG - VAVFNDNLRNALDGNVFDSSAOGFATGATGLTDAIKNGVEGSINDFTSSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                PVFASNSVDETDPTQD-NWGYDPRNYDVPEGQYATNA-NGNARIKEFKEMVLSLHREHIG
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                                                     TPSEVIGFHY-HHIAKWGPWDEMVVLHNGGGDKVDIRLPASGEWEVIVDGKKAGLVPLYT
                                                                                                                                                                          QAIQYVEAHDNHTLWDKLQFVFPDEEEEEVLRACHRLATAIVLTSQGIPFLHGGQEFFRTK
                                                                                                                                                                                                    ETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXK
                                                                                                                                                                                                                                                                                           TYWASEYRVDGFRFDLMGIIDQMTMKEVKRALAPINRQILLLGEGWDLET-PLENDQKTT
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                                                                                                                                                                                                                                   LAQARAVPFLHFFHDTFRDAVKGSTFDLNKGGFCAGNIELKETLIASMLGHEAQF-DRPS
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1084.5;
Pred. No. 1.1
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RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S. K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S. K., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Choi S. K., Codani J.J., Conner S., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Moone D., O'Railly M., Ogawa K., Ogiwara A., Odega B., Park S.H.,
RA Noone D., O'Railly M., Ogawa K., Ogiwara A., Odega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Pesecan E., Pujic P., Varielle B., Rapport G., Rey M., Reynolds S.,
RA Sekiguchi J., Sekowska A., Serros F., Scoffone F.,
RA Sekiguchi A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambut R., Wedler F., Wedler H., 
                                      Matches
                                                        Query Match
Best Local
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O34587;
O1-JAN-1998 (
O1-JAN-1998 (
O1-MAY-2000 (
AMYX PROTEIN.
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Azevedo V., I
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Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                    Viari A., Wambuit R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamot M., Yamane K., Yashida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danet The complete genome sequence of the gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                        EMBL; AF008220; AAC00283.1;
EMBL; Z99119; CAB14971.1; -.
INTERPRO; IPR000461; -.
                                                                                                                                                                                                                                Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98044033; PubMed-9384377;
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                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Nature
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  234 EGNYQYKVALNDSWNNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVES 293
                                                                                                                                      PF00128; alpha-amylase;
NCE 718 AA; 81104 MW;
                                                                                                                                                                                                                                                                                                                                390:249-256(1997).
                                                        Similarity
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                                        Conservative
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                                    Score 1039.5;
Pred. No. 5.8e
25; Mismatches
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96F9EB7667877E93
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                                    .5; DB 2;
5.8e-55;
hes 272;
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databases
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bacterium
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                                    Gaps
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE BI-FUNCTIONAL PROTEIN (SECRETED ALPHA-AMYLASE/DEXTRINASE)
SC10B7.21C.
                                                                                                                                                                                                                                                            Q9KZ11
                                                                                                                                                     Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
STRAIN-A3(2);
Cerdeno A.M., Parkhill J.,
Submitted (MAY-2000) to the
                                                               STRAIN-A3(2);
Seeger K.J., Harris |
Submitted (MAY-2000)
                                                                                                                             Actinomycetales;
NCBI_TaxID=1902;
                                                                                                     SEQUENCE FROM N.A.
                                       SEQUENCE FROM N.A.
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SEQUENCE FROM
STRAIN-A3(2);
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL355752; CAB90874.1;
EMBL; AL355752; CAB90874.1;
SEQUENCE 1798 AA; 194106 MW; 43D13868FACF5C6A CRO
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                            VLYGEGWNFGEVA-
                                                        ALYGEPWTGGTSALPDDQLLTKGAQK---GMGVAVFNDNLRNAL-DGNVFDS--SAQGFA
                                                                                   VKALNEDGLRVVMDVVYNHTAASGQAKTSVLDRIVPGYYQRLLADGSVANSTCCS-NTAT
                                                                                                                                                                                                      PDCDLAALPAGSEKQQECVTKAAAKDAFNWGYDPYHYTVPEGSYATDPDGTERTVEFRKM
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
ALKALINE AMYLOPULLULANASE.
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STRAIN-C-125 / JCM 9153;
Takani H., Nakasone K., Takaki Y.;
Takani H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001519; BAB07416.1; -.
SEQUENCE 1072 AA; 120674 MW; 5264235CF24619D9 CRC64;
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Bactilus halodurans.

Bacteria; Firmicutes; Bactilus/Clostridium
Bactilus/Staphylococcus group; Bactilus.

MCBI_TaxID-86665;
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                                      NYQYKVALNDS-----W-NNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPN
                                                                                                                VKDASLGQDVT-AVLAGTFQHIFGGSDWAPDNHSTLLKK-----VTNNLYQFSGDLPEG
                                                                                                                                                       ANPFSDEQTSRYGAYLDVELADDANEI------GFLVVNRENGDKD-----
                                                                                                                                                                                           -----NAYLDA-----SNQVLVKLSQPLTLGEGXSGF-TVHDDTANKDIPVTS
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165; Mismatches 402; Indels 29
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                                                  ALKALINE AMYLOPULLULANASE.
Bacillus sp.
Bacteria, Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1409;
  SEQUENCE FROM N.A. STRAIN-KSM-1378;
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Last sequence update)
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QLGITHVQLMPVFASNSVDE------TDPTQDNWGYDPRNYDVPEGQYATN-ANG
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GPPPHAGEKGKPDHASK 1070
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J. Biol. Chem. 271:24075-24083(1996).
EMBL; D78258; BAA11332.1; -.
HSSP; P06278; IVJS.
INTERPRO; IPR000461; -.
INTERPRO; IPR000833; -.
INTERPRO; IPR001833; -.
INTERPRO; IPR001899; -.
PPAM; PP00128; alpha-amylase; 2.
PPAM; PP00128; alpha-amylase; 2.
PPAM; PP00128; alpha-amylase; 2.
PPAM; PP00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
SEQUENCE 1938 AA; 214917 MW; A29D3F715EB6A72E CRC64;
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Hatada Y., Igarashi K., Ozaki K., Ara K., Hitomi J., Kobayashi T.,
Kawai S., Watabe T., Ito S.;
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hes 284; Conservative 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIIVHYFCPAGDYQPWSLWMW-----PKD----GGGAEYDFNQPADSFGAVASADIPGNPS 86
                                                                                                                                                                                                                                                      GMKNK---GKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPV---FASNSVDE----
                                                                                                                                                                                                                                                                                                IAP-NGTRG-----MIVDLAKTDPAGWNSDKHITP--KNIEDEVIYEMDVRDFSIDPNS 475
                                                                                                                                                                                                                                                                                                                                                                      KVDQNEVVDTIEMVKGDRGVWSVKLTKDNTGLDSLKGYYYHYEITHGDVTNLALDPYAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                           RTISVKS-GWK------LIDEMYAYDGKLGAELHEDGTATLKVWSPKADNVSVVLYD 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINLTV------------PA 262
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GEDLKAQFGTFASFVEK-----LDYIQELGVTHIQLLPVMSYYFSNEFESGERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYD 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EDANK-IGELEVNKQSGGQTGDMTFDMLKQYNQLFVKEGED------K 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGFTVHDDTANKDIPVTSVKDASLGQ--DVTAVLAGTFQHIF--GGSDWAPDNHSTLLKK 220
                                                                                                            NHTFATQISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEY 640
                                                                                                                                                    LEYASTGTNYNWGYDPHNYFSLSGMYSENPEDPELRIKEFKNLINEIHKRDMGVVLDVVF
                                                                                                                                                                     ----TDPTQDNWGYDPRNYDVPEGQYATN-ANGNARIKEFKEMVLSLHREHIGVNMDVVY 580
                                                                                                                                                                                                                                                                                                                                                                                                          SA-TGSVTKIVPMTASGHGVWEATVNQ-----NLENWYYMYEVTGQGSTRTAVDPYATA 424
                                                                            NHT - - AQVHIFEDLVPNYYH - FMDADGTPRTSFGGGRLGTTHEMSRRVLVDSIKHWVDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DVTIE-GEKTVHVHGEFDLEKIPFSVTY-----LD 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 817.5; DB 2;
Pred. No. 7.4e-41;
3; Mismatches 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1938;
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	TP 118	100 GVSGGDTLALEEVEGGL	Db	
	NINLTVP 261	202 HIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINLTV :	Qy	
	99	59 KOQQAIMLSRDLIVVKPALAQPGAWLTLHVSPTATLKLGAD	Db	
	VLAGTFQ 201	147 SNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKDASLGQDVTAVLAGTFQ	Qy	
	VRTVGDL 58	7 KLGFIVHKGD-DKDPGPDGTLTREQGNQLWIVSGNPTPSTTRPDTR	Дb	
	AVSNAYLDA 146	WTKDVSADRYIDLSKGNEVWLVEGNSQIFYNEKDAEDAAKP	Qy	
ω A)10; 247; Gaps	ry Match 16.1%; Score 815.5; DB 2; Length 9 t Local Similarity 26.9%; Pred. No. 3.1e-41; ches 260; Conservative 126; Mismatches 332; Indels	Quer Best Matc	
		SEQUENCE 910 AA; 97926 MW; FEAA466078F9A504 CRC64;	ເກ ⊢	
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		The Radioresistant Bacterium		
	umann R.D.,	L., Daly M.J., Minton K.W., F. E., Salzberg S., Smith H.O.,		
	Ki C.,	J., Lam P., McDonald L., Utterb		
	D.L	n R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardso		
	on J.D.,	en J.A., Heidelberg J.F., Hickey E.K., Peters		
			RC S	
		[1]		
	occus.	Hacteria; Thermus/Deinococcus group; Deinococcales; Deinococ NCBI_TaxID=1299;		
		us radiodurans.		
		ALPHA-GLU		
		(TrEMBLrel. 14, Last annotatio		
		2000 (TrEMBLrel. 13, Created) 2000 (TrEMBLrel. 13, Last sequence up	DI DI	
		0 Q9RXBO PRELIMINARY; PRT; 910 AA.	Q9RXBO	
		.T 10	SUL	
		1816 QEGTDPGDGDGDGNTPPPG 1834	Db 1	
		926 STLGQAEGSVQVPG 939	Qy	
	VVVRVGE 1815	756	Db 1	
	KWAINATSGKVGE 925	- G	Qy	
	GVEYYTF 1755	696 TRDYTAGLIELRRSSDAFRLGSRELVDSNVTMVDA	Db 1	
	NTVAYELTDH 885	842YYSGLIHLRLDHPAFRWTTANEINSHLQFLNSPENTV	QY	
	YP-VNNV 1695	1637 QWRAPATEAPYKSTYMTDADGNPFVYPYFIHDSYDSSDIINRFDWEKATDAEKYP-VNNV	Db 1	
	-QYPDVFN- 841	GGNDNSYNAGDAVNEFDWSRKA	Qy	
	QEFGRTK 1636	1577 IEAHDNUTUYDVIAQSIKKDPEIAENDLEIHKRIRVGNAMVLTSQGTAFLHAGQEFG	D b 1	
	EEMLRXK 812	NPNDSEADRIKMDELAQAVVMTSQGVPFMQGG	ОУ	
	PGDVVQY 1576	1517 TEAVGSFSDEFRNELKSGFGSEGQPRF1TGGAVNVQQIFDNIKAQPHNFMADQPGDVVQY	Db 1	
	PGETINY 757	699 GMGVAVFNDNLRNALDGNVFDSSAQGFATGATGLTDAIKNGVEGSINDF-TSSPGETINY	Qy	

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ID 064
AC 064
AC 064
DT 011-
DT 01-
DT 01-
DT 01-
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DT 01-
ELM
COC MASS
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O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence upda
O1-MAY-2000 (TrEMBLrel. 13, Last annotation up
STARCH DEBRANCHING ENZYME.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnollophyta; Liliopsida; Poales; Poaceae; Or
    Francisco
                STRAIN-CV.
                             SEQUENCE FROM N.A.
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 P.B., Zhang
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                NORIN-8;
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  Park
                                                                                                                             Last sequence update)
Last annotation update)
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s.,
 Ogata
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                                                                       Tracheophyta; Spermatophyta; ceae; Oryza.
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  Yamanouchi
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Best Local Similarity
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB012915; BAA28632.1; -.
MENDEL; 28470; Orysa;2480;28470.
INTERPRO; IPR000461; -.
PFAM; PFO0128; alpha-amylase; 1.
SEQUENCE 988 AA; 109858 MW; 9D537693EF154A4E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------DPTQD-------NWGYDPRNYDVPEGQYATNANGNARIKEFKEMYL 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AWNVNDQDTSLFLYASRDATMHVSDGAIHGYDSKIELEPEHASLPDNVAEKFPEIRS---
                                                                                                                                                                                                                                                                                                                                       LYGEGWDFGEVAONKRGINASOI----NMSGTGIGSFNDRIRDSVNGGNPFGNPLQQGFS
                                                                                                                                                                                                                                                                                                                                                                      LYGEPWTGGTSA-----LPDDQLLTKGAQKGMGVAVFNDNLRNALD-GNVFDSS-AQGFA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNQNLENWYYMYEV-----TGQGSTRTAVDPYATAIAPNGTRGMIVDL--AKTDPAGWN
KDAQNEKCKMAQLDKNFSYVVTIFNVCPHEVSIEIHDLASLGLELHPIQVNSSDALVRQS
                               TDHVNK-----DK-WGNIIVVYN--PNKT-----VATINLPSGKWAINATSGKVGES
                                                                                                                                                                    FMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS---------------
                                                                                                                                                                                                     GSPVGYTSSPVETINYVSAHDNETLFDIVSIKTPIGLSIDEKCRINHLASSMIALSQGIP 784
                                                                                                                                                                                                                                       ----FTSSPGETINYVTSHDNYTLWDKIALSNPNDSEAD-RIKMDELAQAVVWTSQGVP
                                                                                                                                                                                                                                                                      TGLFLEPNGYYQGNEADTRRELAT-YADHIQIGLAGNLKDYVLRTHTGEAKKGSDIYTFD
                                                                                                                                                                                                                                                                                                      TG--------ATGLTDAIKNGVEGSIND--------
                                                                                                                                                                                                                                                                                                                                                                                                         HFMVDRLTVDDLLNWAINYKVDGFRFDLMGHIMKSTMIRAKSAIRSLTRDVHGVYGSKIY
                                                                                                                                                                                                                                                                                                                                                                                                                                         RPMVQKEIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAAS-----ELHAI-NPGIA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLHREHIGVNMDVVYNHTFAT - - - - QISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSPPITKHPGRIMETVMQDSAGIRHLRKLSAAGLTHVHLLPSFHFASVDDNKSNWKFVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSDEEPNLESFSDISIYELHIRDFSAHDSTVDCNS----RGGFVHLHFRLFRLNLLNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SDKHITPKNIEDEVIYEMDVRDFS----IDPNSGMKNKGKYLAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPRYPENQYYLYEVKVYHPSTSQVEKCLADDPYARGLSANGTRTWLVDINSETLKPASWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DMFAYTG-PLGAVFSDKDVDLYLWAPTAQDVRVCFYDGPAGPLLQTVQLKEL-NGVWSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTASGHGVWEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -YRTFRVPSS-VDVASLVKCQLAVASYDAHGRHQDVT-----GLQLPGVL-----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYDTINNPNADLQVESGYKTDLYTYTL --- GEDPDVSHTLSIQTDGYQAKQVIPRNVLNS 334
                                                                  PSFRPLKNHILSAFDNFVDILKIRYSSPLFRLSTASDIEQRVRFHNTGPSMVPGVIVMSI
                                                                                                  ---- RKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSPEN----TVAYEL
                                                                                                                                     FFHAGDEILRSKSLDRDSYNSGDWFNKLDFTYETNNWGVGLPPRDKNEENWHLIKPRLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TEKGTKGPDNV-----KTGIDSLKQL---GITHVQLMPVFASNSVDET------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.9%; Score 805; DB 10; 27.6%; Pred. No. 1.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 250;
                                                                                                   882
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938 976

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RESULT

0816 38

ID 0816 38

ID 010 01-

D7 01-

D7 01-

D7 01-

D7 01-

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Best Local Similarity
Matches 262; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O81638 PRELIMINARY; PRT; 962 AA.
081638;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PULLULANASE-TYPE STARCH DEBRANCHING ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beatty M.K., Rahman A., Myers A.M., James M.G.;
"Genetic and biochemical characterization of ZPU1, a pullulanase-type starch debranching enzyme from maize.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF080567; AAD11599.1; -.
MENDEL; 32273; Zeama; 2480; 32273.
SEQUENCE 962 AA; 106239 MW; 5F5AAB7C6EBD5D10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays (Maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
NCBI_TaxID-4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-ENDOSPERM;
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      523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 AAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKDASLGQDVT 193
                                                                                                                                                                                                                                                                                                                                                               350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AVLAGTFQHIFGGSDW-APDNHSTLLKKYTNNLYQFSGDLPEGNYQYKVALNDSWNNSYP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
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                                                                                                                                                                                                                                                                                                                                                         ERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAI------NPGI 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARGLSANSTRTWLVDINNETLKPLAWDGLAAEKPRLDSFSDISIYELHIRDFSAHDSTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAIAPNGTRGMIVDL--AKTDPAGWNSDKHITPK--NIEDEVIYEMDVRDFSI-DPNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDVT-----GLQLPGVL------DDMFAXTG-PLGTIFSEEAVSMYLWAPTAQDVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLYDSATGSVTKIVPMTASGHGVWEATVNQNLENWYYMYEV-----TGQGSTRTAVDPY 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLIA-----WNISDQKTSLFLYASRNATMCMSSQDMKGYDSKVELQPE-NDGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APRPPMATAEEGASSDVGV-----AVAESAQGFLL-------DARAYWVTK
                                                                                                                    QALNRLGLRVVMDVVYNHLYSSGPFAITSVLDKIVPGYYLRRDSNGQTENSAAVN-NTAS
                                                                                                                                                                               LSLHREHIGVNMDVVYNHTFATQ----ISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDNINLTVPAGGAHVT--FSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTL---GED 307
EHFMVDRLIVDDLLNWAVNYKVDGFRFDLMGHIMKKTMIRAKSALQSLTIDEHGVDGSKI
                                                                                                                                                                                                                                           ELSKLPPGSDLQQAAIVAIQEEDPY--NWGYNPVVWGVPKGSYASNPDGPSRIIEYRLMV
                                                                                                                                                                                                                                                                          Conservative 143; Mismatches 325; Indels 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VTQKEPEISS----YRAFRIPSS-VDVATLVKCQLAVASFDAHGNR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.8%; Score 797; DB 10; 27.0%; Pred. No. 4.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 962;
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YRTFRVPSS-VDVASLVKCQLAVASYDAHGRHQDVTGLQLPGVLD 196	153 -YRTFRV	В
INNPNADLQVESGVKTDLVTVTLGEDPDVSHTLSIQTDGVQAKQVIPRNVLNS 334	278 VYDTINN	Qγ
AWNVNDQDTSLFLYASRDATMHYSDGAIHGYDSKIELEPEHASLPDNVAEKFPFIRS 152	96 AWNVNDQ	В
YPSDNINLTVPAGGAHVTFS	246 SWNNS	Qy
15.7%; Score 793; DB 10; Length 986; Similarity 27.6%; Pred. No. 8e-40; 51; Conservative 134; Mismatches 277; Indels 248; Gaps 37	Query Match Best Local Simi Matches 251;	Que Bes Mat
À	EQUENCE 9	SQ
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(PROOO461; 28: alpha-amvlase: 1.	PEAM: PF0012	R R
)EL; 16402; Orysa; 2480; 16402.	MENDEL; 1640	DR
209-216(1996).)2; BAA09167.1;	EMBL; D50602	
	gene.";	
perm: purification, cDNA and chromosomal localization of the	rice endospe	
Y., Yano M., Sasaki T.;	"Starch debr	
	MEDLINE-9627	
SEQUENCE FROM N.A.	STRAIN=CV F	7 7 7
NCB1_1dX1U=4030;	[1]	RN
	Magnol tophyt	88
<pre>Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;</pre>	Eukaryota; V	88
ANCHING ENZYME PRECURSOR.	STARCH DEBRA	E
(Trembirel: 03, Last sequence update)	01-MAY-2000	D E
(Trembirel 03, Created)	01-MAY-1997	3 5
	P93416;	٦.
DRRITHINARY. DRT. 086 AA	16	P9341
	LT 13	RESUL
ETVP 950	941 DTATGRETV	Db
866 dADAR	929 GQAEGSVQVP	Qy
IDETFSCVVTVFNVCPYEVSIEIPDLASLRLQLHPVC	881 ARNDRHDMAQ	망
KDKWGNIIVVYNPNKT		Qy
IDITAALDKFIDILKIRYSSPLERLTTASDIVQRVHFHNTGPSLVPGVIVMSIED 880	821 FKPAKHD	В
DVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSPENTVAYELTD 884	838D	Qy
HAGDEILRSKSLDRDSYDSGDWFNKIDFTYETNNWGVGLPPREKNEGSWPLMKPRLENPS 820	761 HAGDEIL	DЬ
QGGEEMLRXKGGNDNSYNAGDAVNEFDWSRKAQYP837	803 QGGEEML	Qy
PVGYASSPIETINYASAHDNETLEDIISLKTPMDLSIDERCRINHLSTSMIALSQGIPFF 760	701 PVGYASS	₽ D
SPGETINYVTSHDNYTLWDKIALSNPNDSEAD-RIKMDELAQAVVMTSQGVPFM 802	747FTSS	Qγ
PNGFYOGNETETRITLATYADHIQIGLAGNIKDYVVISHTGEARKGSEIRTFDGS 700	641 GLFLEPN	망
ATGLTDAIKNGVEGS	728 G	Оу
YLYGEGWNFGEVAENQRGINGSQLNMSGTGIGSFNDRIRDAINGGSPFGNPLQQGFST 640	583 YLYGEGW	DЪ
DQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSA	673 ALYGEPW	Qy

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RESULT 14
Q95758
ID Q95758
AC Q95758
AC Q95758
DT 01-MAY
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE 99169277; Pubmed 10069825;
Thana X.Q., Himova M.,
                                                                                                                                                                                                                                                                                                                         09S7S8;
                                                                                                      Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
MCBI_TaxID-4513;
                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrcl. 01-MAY-2000 (TrEMBLrcl. 01-MAY-2000 (TrEMBLrcl. LIMIT DEXTRINASE.
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                                                                                                                                                                                                                                        (TrEMBLrcl. 13, Created)
(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 13, Last annotation
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Best Local Similarity 27.8%;
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EMBL: AF122050: AAD34348.1; -.
EMBL: AF122049; AAD34347.1; -.
Hydrolase; Clycosidase.

Hydrolase; Clycosidase.
SEQUENCE 962 AA; 105752 MW; 5158386FAED162EE C
                              897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 FSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLSIQTDGYQAKQVIP 328
                                                                                                                                                                                                            YTLWDKIALSNPNDSEAD-RIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAG
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VFNVCPHEVSMDIPALASMGFELHPVQVNSSDTLVRKSAYESATCRFTVPGRTVSV
                            VYN--PNK-----TVATINLPSGKWAINATSGKVGESTLGQAEGSVQVPGISMMI 944
                                                           IRYSSPLERLSTANDIKQRVREHNTGPSLVPGVIVMGIEDARGESPEMAQLDTNESYVVT
                                                                                              LRLDHPAFRMTTANEINSHLQFLNSPENTVAYELTDHVNKDK------WGNIIV 896
                                                                                                                              DWFNKLDFTYETNNWGVGLPPSEKNEDNWPLMKPRLENPSFKPAKGHILAALDSFVDILK
                                                                                                                                                             DAVNEFDWS ----
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Pred. No. 1.8e-39;
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RESULT 048541 ID 048

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Best Local Similarity
Matches 233; Conserv
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
LIMIT DEXTRINASE.
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Eukaryota; Viridiplantae; E
Magnoliophyta; Liliopsida;
MCBI_TaxID-4513;
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INTERPRO; IPR000461; -. PFAM; PF00128; alpha-amylase; 1.
SEQUENCE 904 AA; 99123 MW; C7116CC2DE99ED03 CRC64;
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WFNKLDFTYETNNWGVGLPPSEKNEDNWPLMKPRLENPSFKPAKGHILAALDSFVDILKI
                                                                                                                                                                                                          T-YADQIQIGLAGNLRDYVLISHTGEAKKGSEIHTFDGLPVGYTASPIETINYVSAHDNE
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                                                    AVNEFDWS------
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; Poales; Poaceae; Hordeum.
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Search completed: April 22, 2001, 09:10:53 Job time: 354 sec

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Result
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Perfect score:
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Maximum DB
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Gapop 10.0 , Gapext 0.5
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879.620 Million cell updates/sec
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ALIGNMENTS

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P82507
                                                                                                                                                                                                                                                               RESULT
                                     Gene encoding pullulanase - derived from recombinant plasmid pMP1 contgene from Klebsiella genus.
                                                                                                                                                                                                                 01-NOV-1990
                                                             WPI; 1988-333488/47.
N-PSDB; N81341.
                                                                                                    31-MAR-1987;
                                                                                                                  31-MAR-1987;
                                                                                                                                                 JP63245676-A.
                                                                                                                                                                 Klebsiella aerogenes.
                                                                                                                                                                                Pullulanase; starch; alcohol prodn.
                                                                                                                                                                                                Pullulanase protein
                                                                                                                                                                                                                                P82507;
                                                                                                                                                                                                                                               P82507 standard; protein; 1096 AA.
                                                                                    (ELED ) DENKI KAGAKU KOGYO KK; (SUNR) SUNTORY LTD
                                                                                                                                  12-OCT-1988
                                                                                                                                                                                                                 (first entry)
                                                                                                    87JP-0078355
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Disclosure; ; p; Japanese.

The pullulanase protein cleaves alpha-1,6-glucoside bonds of starch and is effective in decomposition of branched starch. It is used in the

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GSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATP 945
                             NMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADJQOPFSRLCEVNSAVKSSEFAGY
                                                                                                                                                                                                                                      \tt dsalkpegwdgltmphaqktkadlakmtiheshirdlsawdqtvpaelrgkylaltaqes
                                                                                                                                                                                                                                              DSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYLALTAGDS
                                                                                                                                                                                                                                                                   dsasgawswqggsdlkgafyryamtvyhpqsrkveqyevtdpyahslstnseysqvvdln
                                                                                                                                                                                                                                                                           DSASGAWSWQGGSDLKGAFYRYAMTYYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLN
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                                                                                                                                                                                                                                                                                                                                                        MLRYTRNALVLGSLVLLSGCDNGSSSSSSS--------GNPDTPDNQDVVVRLPDVA 49
                                                                                                                                                                                                                                                                                                       VQTAGVLDDAYAEAAEALSYGAQLADGGVTERVWAPTAQQVDVVVYSADKKVIGSHPMTR
                                                                                                                                                                                                                                                                                                                            kltpttvnqqvsmrfphlasypafklpddvnvdellqgddgglaes-dgilslshpgadr
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ucose. Amino
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a fragment of a novel Zea mays pullulanase protein. This protein and the encoding nucleic acid fragments may be used to create transgenic plants in which corn pullulanase is present in cells at levels differing from the norm, or in cell types or developmental stages where it is not normally found, in order to alter starch structure in those cells. They may also be used to isolate cDNAs and genes encoding homologous pullulanase from the same or other plant species, to amplify those genes and to produce antibodies for screening of cDNA expression
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DB; V65118.
SDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDNL 417
                                                                                                                                                                                                                                                                                                                                                 qkfpfissyrafripssvdvatlvkcqlavasfdahgnrqdvtglqlpgvlddmfaytg- 121
                                                                                                                                                                                                                                                                                                                                                                            MREPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQTAGVLDDAYAEAAE
                                                                                                                                                                                                                                                                                                                                                                                                          araywvtksliawnisdqktslflyasrnatmcmssqdmkgydskvelqpendglpssvt
                                                                                                                                                                                                                                                                                                                                                                                                                                     AEAHWVDKNTLLWPGGQDKPIVRLYYSHSSKVAADGEG-KFTDRYLKLTPTT--VSQQVS
                                                          aglthvhllpsfqfggvdd------iks-----nwkcvdeie
                                                                                                                                               SGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEV-
                                                                                                                                                                                                    TMPHAQKTKAD-LAKMTIHESHIRDLSAWDQTVPAELRGKYLALTAGDSNMVQHLKTLSA 476
                                                                                                                                                                                                                                  rnwenryylyevtvyhqttgniekclaadpyarglsanstrtwlvdinnetlkplawdgl
                                                                                                                                                                                                                                                                                         --plgtisseeavsmylwaptaqdvsvsfydgp----agplletvqlnelngvwsvtgp
                                                                                                                                                                                                                                                                                                                      ALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTR----DSASGAWSWQGG
                                                                                                                                                                          PONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.2%; Score 1419.5; DB 20; 35.7%; Pred. No. 3.5e-99; tive 172; Mismatches 340; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
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host cell
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Gaps

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SAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPD---

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This partial sequence represents a novel debranching enzyme isolated Zea mays (maize). This enzyme has been used in the production of
                                   Claim
                                                      DNA encoding maize de-branching starch in transgenic plants
                                                                                      WPI; 1997-458572/43, N-PSDB; T93875.
                                                                                                                                                                                      07-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                  Z. mays
                                                                                                                                                                                                                                                                                                                                                                                             W34878
                                                                                                                                                                                                                                                                                                                                                                                                                W34878 standard; Protein; 558
                                                                                                                      Emmermann
                                                                                                                                            (PLAN-) PLANTTEC BIOTECHNOLOGIE
                                                                                                                                                                 07-MAR-1996;
                                                                                                                                                                                                           11-SEP-1997
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                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                    industrial
                                                                                                                                                                                                                                                                                                                            debranching enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGVQIAADGTVTLPAWSVAVLELPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTVDDCMKAG----ASLDSRLDGLVVAINAAP--ESRTLNEFAGETLQLSAIQQTAGENSL 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lenpsfkpakhdilaaldkfldilkiryssplfrlttasdivgrvhfhntgpslvpgviv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glpffhagdeilrsksldrdsydsgdwfnkidftyetnnwgvglppreknegswplmkpr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qgfstglflepngfyqgnetetrltlatyadhiqiglagnlkdyvvishtgearkgseir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGIGSGAGVLPNELASLSDDQVR----HLADLTRLGMAGNLADFVMIDKDGAAKKGSEI-
                                  ļ,
                                                                                                                                                                                                                                                                                                                                                 debranching
                                Page 19-21; 13pp; German.
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                                                                                                                                                                                                                                                                                                                   product.
                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                      Kossmann
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                                                                                                                                                                                                                                                              Location/Qualifiers
1..558
                                                                                                                                                                                                                                                                                                                             maize;
                                                                                                                                                                                                                                                                                                                                                  enzyme
                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                                                                                                                                   "partial sequence of debranching
                                                                                                                     Willmitzer L;
                                                                                                                                                                                                                                                                                                                            transgenic plant;
                                                                  enzyme
                                                                                                                                            GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1078
                                                                  useful for
                                                                                                                                                                                                                                                                                                                            starch;
                                                               production
                                                                                                                                                                                                                                                                                                                            food industry;
                                                                                                                                                                                                                                                   enzyme'
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                            starch; sugar production; maltodextrin.
                                      Pullulanase; pulB; debranching enzyme; amylopectin; thermostable; genetically engineered variant; wheat; potato; wheat; manioc; rick starch; sugar production; high fructose syrup; high maitose syrup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic plants in which the nucleic acid is stably integrated in host cell's genome and expressed. Such an enzyme can be used in the production of starch which is useful in the food industry or in the production of industrial products e.g. paper, adhesives, textiles, textile care products, building materials, soil stabilisers, agrochemicals, pharmaceutical products, cosmetics, coal briquettes, flocculants for ore and coal slurries, foundry sand binders, rubber
                                                                                                        Pullulanase (pulB)
                                                                                                                                         05-MAY-2000
                                                                                                                                                                                                     Y78513 standard; protein; 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 SDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAIKQ 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 DLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRM 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 -lglrvvmdvvynhlyssgpfaitsvldkivpgyylr-rdsngqtensaavnntasehfm 122
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                                                                                                                                                                                                                                                                                                                 ADGTVTLPAWSVAVLELPQ 1078
                                                                                                                                                                                                                                                                                                                                               ndrhdmaqldet fscvvtvfnvcpy evsie ipdlaslrlqlhpvqvnssdalarqs aydt\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gyasspletinyasahdnetlfdlislktpmdlsidercrinhlstsmialsqglpffha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVRMQAVSLATVMLGQGIAFDQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          egwnfgevaengrgingsglnmsgtgigsfndrirdainggspf--gnplg--ggfstgl
                                                                                                                                                                                                                                                                                                                                                                                                            PGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGM 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGM-PRISDDGSNYEVITRVKEMVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGWDSN---QSDRFEIASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGA 770
                                                                                                                                                                                                                                                                                                                                                                                KAG---ASLDSRLDGLVVAINAAP--ESRTLNEFAGETLQLSAIQQTAGENSLANGVQIA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gdeilrsksldrdsydsgdwfnkidftyetnnwgvglppreknegswplmkprlenpsfk 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558 AA;
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                                                                                                                                        (first
                                                                                                        amino acid
                                                                                                                                        entry)
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Pred. No. 2.2e-67;
0; Mismatches 198;
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                                                                                                        sequence
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Bacillus acidopullulyticus

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Best Local S
Matches 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parent enzyme. The enzyme variants are useful for converting starch to one or more sugars. This is useful when starches such as corn, potato, wheat, manioc and rice starch are used as starting materials in commercial large scale production of sugars, such as high fructose syrup, high maltose syrup, maltodextrins, amylose, G4-G6 oligosaccharides and other carbohydrates such as fat replacers. The thermostable debranching enzymes of the invention make it possible to perform liquefaction and debranching simultaneously before the saccharification step. By debranching using the thermostable debranching enzyme variants during liquefaction together with the action of an alpha-amylase, the formation of panose precursors is reduced, thereby reducing the panose content in the final product and increasing the overall saccharification yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a pullulanase amino acid sequence. Pullulanases are debranching enzymes which can attack amylopectin. This sequence represents a parent enzyme from which genetically engineered variant debranching enzymes can be created. The genetically engineered enzyme has an improved thermostability at a pH in the range of 4-6 compared to the parent enzyme. The modified enzyme may alternatively or also have an increased activity towards amylopectin and or glycogen compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 29; Fig 3; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Variant bacterial pullulanases and isoamylases having, e.g. increased thermostability, used for converting starch from potatoes into high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                    78
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                                                                                                                                                                                                                                                                                        ndwsqkntsddlhi---dltkgheiwivqgdpniyynlsda-qaaatpkvsnayldnekt
wklkvpgnlknwyylyqvtvngktqtav-----dpyvraisvnatrgmivdledt--np
                                  WSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKP 411
                                                                                                                                                                            LPDNANVDELLQGETVAIAAAEDGILISAT-QVQTAGV----
                                                                                                                                                                                                                  vl-----akl---tnpmtlsdgssgft----vtdkttgeqipv-----taat 191
                                                                                                                                                                                                                                                                                                                                                                                                  ADYSSKNLYLWNNETCDALSAPVADWNDVSTTPSGSDKYGPYWVIPLNKESGCINVIVR- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-160767/14.
                                                                                                        LDDAYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGA
                                                                                                                                          nansassseqtdlvqltlasapd---vshtiqvgaagyeavnliprnvlnlpryyysgnd
                                                                                                                                                                                                                                                    LLWPGGQDKPIVRLYYSHSSKVAADGEGKFTDRYLKLTPTTVSQQVSMRFPHLSSYAAFK
                                                                                                                                                                                                                                                                                                                            -DGTDKLIDSDLRVAFGDFT-DRTVSVIAGNSAVYDSRADAFRAAFGVALAEAHWVDKNT
                                                                                                                                                                                                                                                                                                                                                              snyanwdlwmwpyq-----pv-ngngaayefsgkddfgvkadvqvpgddtqvglivrt
                                                                       Ignvysnkata-
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Pred. No. 3.8e-55;
70; Mismatches 337;
                                                                  frvwaptasdvqlllynsetgpvtkqlemqksdngt
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                         01-APR-1996;
                                                01-APR-1996;
                                                                                                  JP09271385-A
                                                                                                                                                               Bacillus
                                                                                                                                                                                       Trimmed enzyme protein
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                                                                           21-OCT-1997.
                                                                                                                         Bacillus sp.
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                                                                                                                                                                                                                                                                                                                              vevpalstiilh--qgtse
                                                                                                                                                                                                                                                                                                                                                                                                                                 ---rkaqfenvfdyyswlihlrdnhpafrmttadqikqnltfldsptn---
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                                                                                                                                                                                                                                                                                                                                                                                                        MKAGASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADGT 1063
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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yme with wide substrate speci
                                                                                                                                                                                   KVIGSHPMT---RDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSL
                                                                      YDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTDRT
                                                                                                                                                                                                                            apngtrgmvvdl--aktnptgwks----dkhmtpkniedeviyemhvrdfsi-dsnsgmt
                                                                                                                                                                                                                                                                                                                                       qtdgfktgrv1prnvldfsqyyysgedl--gntytkkattfkvwaptstkvnvllyn---
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                           SVLDKIVPWYYORLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFD
                                                                                                                                                                      nkgkylaltekgtkgpenvktgvdslkqlgithvqlqpvfafnsvde--------
                                                                                                                                                                                                                                                      STNSEYSOVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAE
                                                                                                                                                                                                                                                                                 kaagaltktvpmkasghgvwsvtvpqnlenwyylyevtgqgstrtav-----dpyatai
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                                                       ydprnynvpegqyatdangttr1kefkemvlslhrnhigvn--mdvvynhtfatqisd--
                                                                                                                                          RLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTD--SYNWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277;
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This sequence represents a pullulanase amino acid sequence. Pullulanases are debranching enzymes which can attack amy lopectin. This sequence represents a parent enzyme from which genetically engineered variant debranching enzymes can be created. The genetically engineered enzyme has an improved thermostability at a pH in the range of 4-6 compared to the parent enzyme. The modified enzyme may alternatively or also have an increased activity towards amylopectin and or glycogen compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pullulanase; debranching enzyme; amylopectin; thermostable; cugenetically engineered variant; wheat; potato; wheat; manioc; starch; sugar production; high fructose syrup; high maltose symaltodextrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1044
                                                                                                                                                                 Variant bacterial pullulanases and isoamylases having, e.g. incohermostability, used for converting starch from potatoes into
                                                                                                                                                                                                                                               Bisgard-Frantzen
                                                                                                                                                                                                                                                                                                           02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                        02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus deramificans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pullulanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-2000
                                                                                                                                                        fructose syrup
                                                                                                                                                                                                                                                                             (NOVO ) NOVO-NORDISK
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                                                                                                                                                                                                                  2000-160767/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMGYHPKAQILSAWERIKALNPDIYFFGEGWDSNQS--DRFEIASQINLKGTGIGTFSDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1kmdelaqavvvtsqgvptmqggeemlrtkggnsnsynagdavnefdws------
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                                                                                                                          Fig 3; 116pp; English.
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Best Local Similarity
Matches 278; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parent enzyme. The enzyme variants are useful for converting starch to one or more sugars. This is useful when starches such as corn, potato, wheat, manioc and rice starch are used as starting materials in commercial large scale production of sugars, such as high fructose syrup, high maltose syrup, maltodextrins, amylose, 64-66 oligosaccharides and other carbohydrates such as fat replacers. The thermostable debranching enzymes of the invention make it possible to perform liquefaction and debranching simultaneously before the saccharification step. By debranching using the thermostable debranching enzyme variants during liquefaction together with the action of an alpha-amylase, the formation of panose precursors is reduced, thereby reducing the panose content in the final product and
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                                                                                                                                                                                                                                                                                                                                                                                               VPAELRGKYLAL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VY-SADKKVIGSHPMTRDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dvshtlsiqtdgyqakqviprnvlnssqyyysgddlgntytqkattfkvwaptstqvnvl
                                                                                                                                                                                                                                                                                                                                                              sgmknkgkylaltekgtkgpdnvktgidslkqlgithvqlmpvfasnsvde-tdptqd--
                                                                                                                                                                                                                                                                                                                                                                                                                                           atalapngtrgmlvdl--aktdpagwns----dkhitpkniedevlyemdvrdfsi-dpn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agdyqpwslwmwpkdgggaeydfnqpadsfgavas--adipgnpsq--------
  DRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLA
                                                                                                                                                                                                                      WGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHSLSTNSEYSQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tsvkdaslgqdvtavlagtfqhifggsdwa----pdnhstllkkvtnnlyqfsgdlpegn
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                                                                             FDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDSNQS--DRFEIASQINLKGTGIGTFS
                                                                                                                  ----fdklvpeyyyrtddagnytngsgtgneiaaerpmvqkfiidslkywvneyhidgfr
                                                                                                                                                            RTSVLDKIVPWYYORLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFR
                                                                                                                                                                                               QPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYN
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                                     fdlmallgkdtmskaaselhainpgialygepwtggtsalpddqlltkgaqkgmgvavfn
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15-JUL-1993;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                             /note= "corresponds to GGN codon"
  Claim
                   New pullulanase from Bacillus deramificans -saccharification etc., with good stability overanges, also related DNA vectors, transformed
                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                              /note=
Misc-difference 620
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                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                   Pullulanase; recombinant production; pullulan;
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus deramificans pullulanase precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ||::: | ||| || || :|| dnlrnal-dgnvfds----saqgfatga--
                                                                        1994-210291/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atsgkvgestlgq----aegsvqvpgismmil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFVMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLA 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIQQTAGENSLANGVQIAADGTVTLPAWSVAVL 1074
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                                                               Q68699
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Fig 5;
                                                                                            DeWeer
                                                                                                                                                                                                                                                                                                                                                                                         alpha-1,6-glycosidic bond; starch saccharification.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                     92BE-0001156.
93BE-0000744.
93BE-0001278.
                                                                                                                  SA.
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812
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                                                                                                                                                                                                                                                                          /note= "corresponds to CAN codon" 621
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 163
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                                                                                                                                                                                                                                             /note-
   French
                                                                                                                                                                                                                                          "corresponds
                                                                                                                                                                                                                                                               "corresponds
                                                                                                                                                                                                                                                                                                        "corresponds to NNA codon"
                                                                                                                                                                                                                                                                                                                                                                      (EMG
                     camificans - for starch stability over wide temp. transformed cells etc.
                                                                                                                                                                                                                                             to ANA codon
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       LASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVN
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                                                                                                                     -KLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDS
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15-JUL-1993;
19-NOV-1993;
This sequence represents the mature pullulanase enzyme isolated from Bacillus deramificans T 89.117D. The pullulanse hydrolyses alpha-1,6-glycosidic bonds of amylopectin and of pullulan. The
                                                             New pullulanase from Bacillus deramificans - for starch saccharification etc., with good stability over wide temp. ranges, also related DNA vectors, transformed cells etc.
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Misc-difference 592
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Misc-difference 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFGD----FT--DRTVSVIAGNSAVYDSR------ADAFRAAFGVALAEAHWVDKN- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----adryidlskgnevwlvegnsqifynekdaedaakpavsnayldasnqvlvklsqpl 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPSGSDKY-----GPYWVIPLNKE------SGCINVIVRDGTDKLIDSDLRV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agdyqpwslwmwpkdgggaeydfnqpadsfgavasadipgnpsqvgiivrtqdwtkdvs- 73
                                                                                                                                             \verb|allgkdtmskaaselhainpgialygepwtggtsalpddglltkgagkgmgvavfndnlr|\\
                                                                                                                                                                                                                                  WYYQRLNETTGSVESATCCSDSAPEHRMFA-----KLIADSLAVWTTDYKIDGFRFDLM
                                                                                                                                                                                                                                                                               PEGSYATDPEGTTRIKEERTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVP
                                                                                                                                                                                                                                                                                                                                          SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
                                                                                                                                                                                                                                                                                                                                                                                 altekgtkgpdnvktgidslkglgithvqlmpvfasnsvde-tdptqd------
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggahvtfsyipsthavydtinnpnad--lqvesgvktdlvtvtlgedpdvshtlsiqtdg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stll-----kkvtnnlyqfsgdlp---egnyqykvalndsw--nnpsypsdninltvpa
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   MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRI
                                                                                     nal-dgnvfds----saggfatgu----
                                                                                                                  DSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVM
                                                                                                                                                                                                     eyyyr-----tmmqv11ptdqv1emk1xaerpmvqkf1ids1kywvneyhidgfrfd1m
                                                                                                                                                                                                                                                               peggyatnangnarikefkemvlslhrehigvn--mdvvynhtfatgisd----fdkivp
                              -----tsspgetinyvtshdnytlwdkialsnpndse-adrik
                                             IDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVR
: | | :| | | | | | | | | | | | ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%; Score 788.5; DB 15; Length 25.4%; Pred. No. 3.9e-51; tive 151; Mismatches 359; Indels
                                                                                                                                                                                                                                                                                                                         ----nwgydprnydv
                                                                                     ----tgltdaikngvegsindf--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DW-NDVST 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                928;
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RESULT
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                                                                                                                                                                                                                                                                                                /note- "encoded Misc-difference 135
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            straight chain amylase alpha-1,6-glucosidase.
                                               New modified pullulanase for saccharification of starch
                                                                                                                                                                                                                                                                /note- "encoded Misc-difference 592
                                                                                                                                                                                                                                                                                                                                                                                               Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                               Y31746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1046 TAGENSLANGVQIAADGTVTLPAWSVAVL 1074
                                                                                                                                                                                                                                                                                                                                             Bacillus deramificans
                                                                                                                                                                                                                                                                                                                                                                     Pullulanase; enzyme engineering; starch; saccharification; straight chain amylase; alpha-dextrin 6-glucano-hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               Y31746
                                                                                                                              04-MAR-1998;
                                                                                                                                              03-MAR-1999;
                                                                                                                                                                                WO9945124-A2
                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                       Misc-difference
                                                                       N-PSDB; X87941.
                                                                              WPI; 1999-540851/45
                                                                                                             (GEMV ) GENENCOR INT INC
                                                                                                                                                               10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     894 kvgestlgq----aegsvqvpgismmil 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFR 985
                                                                                               BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                               deramificans
                                                                                              Shetty JK;
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                              98US-0034630
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783
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99..92
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                                                                                                                                                                                              "N-truncated composition
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                                                                                                                                                                                                                                                                                                                                                                                              pullulanase
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                                                                                                                                                                                                                                                                               CAN"
                                                                                                                                                                                              pullulanase used of Claim 32 (see
                                                                                                                                                                                                                     pullulanase
of Claim 31
                                                                                                                                                                                                                      used
(see
                                                       aqueous
                                                                                                                                                                                                                      in claimed Y31747)"
                                                                                                                                                                                              in claimed Y31748)"
                                                      liquefied
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The present sequence represents Bacillus deramificans strain T89.117D mature pullulanase (EC-3.2.1.41). This enzyme has $\mathfrak a$ 4.1-4.5, has a half-life of about 55 hr at 60 deg C and is $\mathfrak a$

s a pI capabl

Claim 31; Fig 1A-E; 49pp; English.

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the recombinant pullulanase appears to be a result of misprocessing of the signal sequence by a signal peptidase as well as susceptibility to extracellular proteolytic processing. The invention provides modified pullulanases, especially N-terminally truncated B. deramificans modified pullulanase (see Y31747-48), nucleic acids encoding them, vectors, host cells and methods for recombinant production. The modified pullulanases are useful in the starch industry for the saccharification of aqueous liquefied starch, forming syrups of high glucose and maltose content. Other uses (not claimed) are: as anti-staling additives in bread; in brewing low calorie beers; production of low calorie foods (where amylose is used as substitute for fat); to clarify fruit juices; in the preparation of oligosaccharides from amylopectin or of tetraholosides from maltose; to condense mono- or oligosaccharides, or in the preparation altose; to condense mono- or oligosaccharides, starch saccharification, the modified pullulanases reduce the amounts of by-products, especially they provide higher glucose them the proparation times, without losses associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of catalysing the hydrolysis of alpha-1,6-glucosidic bonds in amylopectin and pullulan. The invention relates to the discountable deramificans pullulanase recombinantly produced in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reversion reaction products. When used with glucoamylase, they make possible a higher level of dissolved solids in the material being treated, resulting in increased productivity and a more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus host is modified yet retains the ability to catalyse the hydrolysis of an alpha-1,6-glucosidic bond. The modification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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515 SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
                                                                                                                                                                                                                                   404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 yqakqv1prnv1nssqyyysgdd1--gntytqkattfkvwaptstqvnv11ydsatgsvt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 stll-----kkvtnnlyqfsgdlp---egnyqykvalndsw--nnpsypsdninltvpa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 ---HL-----SSYAAFKLPDNANVDELLQGET-----VAIAAAEDGILISATQVQTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 -TLLWPGGQDKPIVRLYYSHSSKVAADGEGKF-----TDRYLKLTPTTVSQQVSMRFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 tlgegxsgftvhddtankdipvtsvkdaslgqdvtavlagtfqhifg----gsdwapdnh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 AFGD----FT--DRTVSVIAGNSAVYDSR-----ADAFRAAFGVALAEAHWVDKN- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 TPSGSDKY-----GPYWVIPLNKE-----SGCINVIVRDGTDKLIDSDLRV 149
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                                                                            altekgtkgpdnvktgldslkqlgithvqlmpvfasnsvde-tdptqd------
                                                                                                                       AL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVN
                                                                                                                                                                                                                           gmivdl--aktdpagwns----dkhitpkniedeviyemdvrdfsi-dpnsgmknkgkyl
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                                                                                                                                                                                                                                                                                                        SQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359;
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Misc-difference 591
04-MAR-1998;
                      03-MAR-1999;
                                                                                                            Misc-difference
                                                                                                                                                                                                         Misc-difference 134
                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                    Bacillus deramificans N-truncated pullulanase.
                                                                                                                                                                                                                                                                                                                                                                           Y31748 standard; Protein;
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                                                10-SEP-1999.
                                                                      √09945124-A2
                                                                                                                                                                                                                                            Bacillus deramificans
                                                                                                                                                                                                                                                                              Pullulanase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nspentvayeltdhvn------kdkwgniivvynpnktvatinlpsgk-wainatsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTGSDQQAGLLVMTVDDGMKAGASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQ 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mdelaqavvmtsqgvpfmqggeemlrxkggndnsynagdavnefdws------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRI
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                                                                                                                                                                                                                                                                             enzyme engineering; starch; saccharification;
                                                                                                                                                                                                                                                                                                                             (first entry)
98US-0034630
                        99WO-US04627
                                                                                                          /note= "encoded by GCN" 783
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Note: The present sequence is not shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vectors, host cells and methods for recombinant production. The modified pullulanases are useful in the starch industry for the saccharification of aqueous liquefied starch, forming syrups of high glucose and maltose content. Other uses (not claimed) are: as anti-staling additives in bread; in brewing low calorie beers; production of low calorie foods (where amylose is used as substitute for fat); to clarify fruit juices; in the preparation of cligosaccharides from amylopectin or of tetraholosides from maltose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an N-terminally truncated pullulanase of Bacillus deramificans strain T89.117D, comprising amino acids 103-928 of the native mature enzyme (see Y31746). The native mature pullulanase (EC-3.2.1.41) has a pI of 4.1-4.5, a half-life of about 55 hr at 60 deg C and is capable of catalysing the hydrolysis of alpha-1,6-glucosidic bonds in amylopectin and pullulan. The invention relates to the discovery that B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pullulanase appears to be a result of misprocessing of the signal sequence by a signal peptidase as well as susceptibility to extracellular proteolytic processing. The invention provides modified pullulanases, especially neterminally truncated B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deramificans pullulanase recombinantly produced in a Bacillus host is modified yet retains the ability to catalyse the hydrolysis of an alpha-1,6-glucosidic bond. The modification of the recombinant
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                                 QQVDVVVY-SADKKVIGSHPMTRDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQY
                                                                                                                                     nnpsypsdninltvpaggahvtfsyipsthavydtinnpnad--lqvesgvktdlvtvtl
                                                                                                                                                                                                    ifg----gsdwapdnhstll-----kkvtnnlyqfsgdlp---egnyqykvalndsw-- 116
                                                                                                                                                                                                                                     AFGVALAEAHWVDKN--TLLWPGGQDKPIVRLYYSHSSKVAADGEGKF-----TDRYLK 230
                                                                                                                                                                                                                                                                     pltlgegxsgftvhddtankdipvtsvkdaslgqdvt----avlag------tfqh
                                                                                                                                                                                                                                                                                                        PLNKESGCINVIVRDGT---DKLIDSDLRVAFG-DFTDRTVSVIAGNSAVYDSRADAFRA 178
tqvnvllydsatgsvtkivpmta-sghgvweatvnqnlenwyymyevtgqgstrtav---
                                                                  gedpdvshtlsiqtdgyqakqviprnvlnssqyyysgddl--gntytqkattfkvwapts
                                                                                                     AEDGILISATQVQTAG------
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                                                                                                                                                                                                                                                                                                                                        13.8%; Score 777; DB 20; 26.8%; Pred. No. 2.4e-50; Live 136; Mismatches 332
                                                                                                   -VLDDA-YAEAAEALSYGAQLADGGVTFRVWAPTA 323
                                                                                                                                                                                                                                                                                                                                                                       Length 826;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atgisd----fdkivpeyyyr-----tmiqviiptdqvlemklxaerpmvqkfiidslk
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                                                                                                                                                                                                                                                                                                            deramificans N-truncated pullulanase
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                                                                                                                                                                                                                                                                   enzyme
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592
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135
                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                       The present sequence represents an N-terminally truncated CC pullulanase of Bacillus deramificans strain T89.117D, comprising CC amino acids 99-928 of the native mature enzyme (see v31746). The CC native mature pullulanase (EC-3.2.1.41) has a pI of 4.1-4.5. a half-life of about 55 hr at 60 deg C and is capable of catalysing CC the hydrolysis of alpha-1,6-glucosidic bonds in amylopectin and CC pullulan. The invention relates to the discovery that B. C deramificans pullulanase recombinantly produced in a Bacillus host CC is modified yet retains the ability to catalyse the hydrolysis of CC an alpha-1,6-glucosidic bond. The modification of the signal CC pullulanase appears to be a result of misprocessing of the signal CC sequence by a signal peptidase as well as susceptibility to extracellular proteolytic processing. The invention provides CC modified pullulanases, especially N-terminally truncated B. C deramificans modified pullulanase, nucleic acids encoding them, CC vectors, host cells and methods for recombinant production. The cC modified pullulanases are useful in the starch industry for the Saccharification of aqueous liquefied starch, forming syrups of CC saccharification of aqueous liquefied starch, forming syrups of CC saccharification of aqueous liquefied starch, forming syrups of CC saccharification of low calorie foods (where amylose is used as substitute CC for fat); to clarify fruit juices; in the preparation of condustry (no details). When used for starch saccharification, the CC modified pullulanases reduce the amounts of by-products, especially
                                                                                                                                                                    Query Match
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Matches 269
                                                                                                                                                                                                                                                                                                                                                              industry (no details). When used for starch saccharification, the modified pullulanases reduce the amounts of by-products, especially they provide higher glucose yields in short reaction times, without losses associated with reversion reaction products. When used with glucoamylase, they make possible a higher level of dissolved solids in the material being treated, resulting in increased productivity and a more energy-efficient process.
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                                        179 AFGVALAEAHWVDKN--TLLWPGGQDKPIVRLYYSHSSKVAADGEGKF-----TDRYLK 230
    76 ifg----gsdwapdnhstli----
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                                                                                                                                                                    Local Similarity 26.8 nes 269; Conservative
                                                                                                       PLNKESGCINVIVRDGT---DKLIDSDLRVAFG-DFTDRTVSVIAGNSAVYDSRADAFRA 178
                                                                                  pltlgegxsgftvhddtankdlpvtsvkdaslggdvt----avlag----
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                                                                                                                                                                                                                                                                       830
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                                                                                                                                                                                                                                                                                                                              deramificans pullulanase sequence given in
                                                                                                                                                                  13.8%; Score 777; DB 20; 26.8%; Pred. No. 2.5e-50; tive 136; Mismatches 332;
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    --kkvtnnlyqfsgdlp---egnyqykvalndsw-- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDSNQS--DRFEIASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----nwgydprnydvpeggyatnangnarikefkemvlslhrehigvn--mdvvynhtf
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                                                                                                                                                                                                                                                                                                                                                                                       FTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSRLDGLVVAINAAPESRT
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GX SX EX BX SX SX S Fervidobacterium industrial saccha Fervidobacterium pennavorans Ven 5 thermostable pullulanase terium pennavorans; saccharification. 5; thermostable pullulanase;

1029

607 789 568 508 671 458

729

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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding Fervidobacterium sp. Ven 5 the pullulanase, useful for industrial saccharification
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N-PSDB; X90036.
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les 243; Conserv
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                                                                                                                                                                                      HIRDLSAWDQTVPAELRGKYLAL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATV 493
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Pred. No. 1.1e-45;
39; Mismatches 315;
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/note= "amylase
834..866
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/note= "N-terminal alpha-amylase"
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/note= "mature amylopullulanase"
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                                                                                                                                                                                                                                                                                                                                                                                  Amylopullulanase (W09255) of Bacillus sp. isolate KSM-AP1378 has N-terminal alkaline alpha-amylase moiety (see also W09256) and a C-terminal alkaline pullulanase moiety (see also W09257). It is the product of an open reading frame in a DNA fragment (T47878) isolated using shotgun cloning and PCR (see also T47879-84). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding alkaline pullulanase having alkaline alpha-amylase activity - useful for improving the efficacy of dish washing detergents and detergents for clothes, esp. on starch soils
1074 leelkeqleikdvdgndvsftdvtiegektvhvhgefdlekipfsvtyldrtisvksgwk 1133
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                            FPHLSSYAAFKLPDNANV---DELLQGETVAIAAAE---DGILISATQV-QTAGV-----
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DB; T47878.
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                               Full length
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                                                                                                                                W73553 standard;
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                                                                                                  W73553;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIDKDGAAKKGSEI--DYNGAPGGYAAD-PTEVVNYVSKHDNQTLWDMISYKASQEADLA 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFV |: :: | | : | | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dhdaesiqiafdeakklnpnivmigegwvtfagdegepvqaadqqwmqyteavgsfsdef 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    edlvpnyyhfm-dadgtprtsfgggrlgtthemsrrvlvdsikhwvdeykvdgfrfdmmg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     edlkaqfgtf----asfvekldyiqelgvthiqllpvmsyyfsnef-----esgerm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AELRGKYLALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -rgvwsvkltkdntgldslkgyyyhyeit-----hgdvtnlaldpyaksmaawnn 1239
                                                                                                                                                                                                                                                                                   rsvstagveyytfvnadtssrtlt--lgqdltegvvvvdaeeanvagvaepagfeltaeg
                                                                                                                                                                                                                                                                                                                 ASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQTAGENSLAN-----GVQIAADG
                                                                                                                                                                                                                                                                                                                                                                                   AELKOMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAG 1007
                                                                                                                                                                                                                                                                                                                                                                                                                    npfvypyfihdsydssdiinrfdwek------atdaekypvnnvtrdyta---- 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  endleihkrir---vgnamvltsqgtaflhagqefgrtkqwrapateapykstymtdadg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ggavnvqqifdnikaqphnfmadqpgdvvqyieahdnltlydvlaqsikkdpeia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHPKAQILSAWERIKALNPDIYFFGEGW----DSNQSDRFEIASQINLKGT-GIGTFSDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eagdkvgkaalvd1--gslgpe-ldyadlpgfekredt1----lyevhvrdfts-dpnlg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E----YSQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TRVRMQAVSLATVMLGQGIAFDQQGSELLRSKS----------
                             Pullulanase protein.
                                                                (first
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                                                                                                                                protein;
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variant; bleach-containing

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Matches 281
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Misc-difference 1050...1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ertnadyegwglwnwed----vespsdgwpngaadaagigkygayydiklkeda 1000
-rgvwsvkltkdntgldslkgyyyhyeit-----
                                             ASGAWSWQ------GGSDLKGAFYRYAMTVYHPQSRKVEQYEVT----DPYAHSLST-NS
                                                                                                                                 -LDDAYAEAAEALSYGAQL-ADGGVTFRVWAPTAQQVDVVVYSA--DKKVIGSHPMTRDS
                                                                                                                                                                               leelkeqleikdvdgndvsftdvtiegektvhvhgefdlekipfsvtyldrtisvksgwk
                                                                                                                                                                                                                             FPHLSSYAAFKLPDNANV---DELLQGETVAIAAAE---DGILISATQV-QTAGV-----
                                                                                                                                                                                                                                                                           -- qynqlfvkegedkvytnpygtvplalvsgevlsd-----klisltftrtegld
                                                                                                                                                                                                                                                                                                                        WVDKNTLLWPGGQDKPIVRLYYS-----HSSKVAADGEGKFTDRYLKLTPTTVSQQVSMR 243
                                                                                                                                                                                                                                                                                                                                                                 nkigflfvn------kqsgggtgdmtfdmlk------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          igflvlnttngdkdggdkavelfspdl--neiwikggsdevflyepvdlpantvrihy--
                                                                                         lidemyaydgk---lgaelhedgtatlkvwspkadnvsvvlydkvdqnevvdtiemvkgd
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Similarity 24.2%; Pred. No. 2.6e-43;
81; Conservative 168; Mismatches 387;
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/note= "nucleotides
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1062 1800	ASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADG	1008 1743	ОУ
1742	AELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAG	948 1702	99 89
947	FTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGE	895	g
1701		1658	8
894	TRVRMQAVSLATVMLGOGIAFDQQGSBLLRSKS	862	do
1657		1601	Vo
861	MIDKDGAAKKGSEIDYNGAPGGYAAD-PTEVVNYVSKHDNQTLWDMISYKASQEADLA	805	Db
1600		1546	Db
804	RDSVRGGGPFDSGDALRQNQGIGSGAGYLPNELASLSDDQVRHLADLTRLGMAGNLADFV : :	745	gy
1545		1528	Qy
. 744	YHPKAQILSAMERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGT-GIGTFSDRL:744	689	99
1527		1468	VQ
688	DKIVPWYYQRLNETTGSVESATCCSDSAPEHRWFAKLIADSLAVWTTDYKIDGFRFDLMG:: : : edlvpnyyhfm-dadgtprtsfgggrlgtthemsrrvlvdsikhwvdeykvdgfrfdmmg	629	DP
1467		1409	Po
628	HYTVPEGSYATDPEG-TTRIKEERTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTDRTSVL:	571	d
1408		1357	Qy
570	CEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPF	511	dq
1356		1340	Yo
510 1339	AELRGKYLALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRL: :	451 1292	ф
450	EYSQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKWTIHESHIRDLSAWDQTVP 450	397	94
1291		1240	64

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            score greater than or equal
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US-08-961-733-11
US-08-961-733-11
US-08-961-733-72
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    US-09-129-075-4
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341 240	SADKKVIGSH KDPSGGE	GAQLADGGVTFRVWAPTAQQVDVVVVS	VQTAGVLDDAYAEAAEALSY : : :	286 191	Db dd
285 190	ETVAIAAAEDGILISATQ : ; ; QLAVAAFSADGACRNATG	PTTVSQOVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQ ::	TPTTVSQQV : DKDQGGLPANVTE	232 135	Db 04
231 134	YLKL : IEGYDVKIKL	DKPIVRLYYSHSSKVAADGEGKFTDR- : YYLFASKTAALKFTDAG	ALAEAHWVDKNTLLWPGGQ	183 85	Db Qy
182	ADAFRAAFGV : L	INVIVRDGTDKLIDSDLRVAFGDFTDRTVSVIAGNSAVYDSRADAFRAAFGV	PLNKESGCINVIVRD	123 53	Db Qy
Gaps 33	964; 3 150;	26.7%; Score 1503; DB 4; Length 36.2%; Pred. No. 9.6e-119; tive 169; Mismatches 324; Indels	itch Pal Similarity 365; Conserva	Query Mat Best Loca Matches	7 m 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CORREST APPLICATION DATA:
                                                                                                                                                                                                                                                                          APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                      STREET:
APPLICATION NUMBER:
                                                                                                                                                   ZIP: 20006
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DERCRVNHLATSILALSQGIPFFHAGDELLRSKSLDRDSYNSGDWFNRLDFSYNSNNWGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·EFAGETLQLSAIQQTAGENSLANGVQIAADGTVTLPAWSVAVLELPQ 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIEDRVRFHNNVPSWIPGLIAMSIEDG-HAGAPGLSQIDPKFQYIVVIINVQPTETKFVN 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPPKDHNESNWPLI---KKRLANPSYKPDKNHIIAAVENFTNLLQIRYSSPLFRLRSAK 855
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SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
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TELEX: 650
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TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano,
                                                                                                                              515
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STLL-----KKVTNNLYQFSGDLP---EGNYQYKVALNDSW--NNPSYPSDNINLTVPA
                                                                                   WYYQRLNETTGSVESATCCSDSAPEHRMFA-----KLIADSLAVWTTDYKIDGFRFDLM
                                                                                                                                                                                                                                                                                                                                              GMIVDL--AKTDPAGWNS----DKHITPKNIEDEVIYEMDVRDFSI-DPNSGMKNKGKYL
                                                                                                                                                                                                                                                                                                                                                                  SQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYL 458
                                                                                                                                                                                                                                                                                                                                                                                                                     KIVPMTA-SGHGVWEATVNQNLENWYYMYEVTGQGSTRTAV-----DPYATAIAPNGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSHPMTRDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEY 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAHVTFSYIPSTHAVYDTINNPNAD--LQVESGVKTDLVTVTLGEDPDVSHTLSIQTDG
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                                                  EYYYR-----TMMQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLM
                                                                                                                            PEGQYATNANGNARIKEFKEMVLSLHREHIGVN--MDVVYNHTFATQISD----FDKIVP
                                                                                                                                             PEGSYATDPEGTTRIKEFRTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVP
                                                                                                                                                                                                                                                                          ALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPVFASNSVDE-TDPTQD------
                                                                                                                                                                                                                                                                                                            AL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVN 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQAKQVIPRNVLNSSQYYYSGDDL--GNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VLDDA-YAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVY-SADKKVI
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                                                                                                                                                                                                    -----NWGYDPRNYDV
                                                                                                                                                                                                                                      SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
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RESULT 3
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                     TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano,
                                                                                                                                                                                                                                          REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DEWEER, PHILIPPE APPLICANT: AMORY, ANTOINE
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                                                                                                       TOPOLOGY:
                                                                                                                  TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 07-JU
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                                                                                   TYPE: protein
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 14.0%;
25.4%;
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CR: 4121-42
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 Score 788.5; DB 1;
Pred. No. 4.7e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMIVDL--AKTDPAGWNS----DKHITPKNIEDEVIYEMDVRDFSI-DPNSGMKNKGKYL
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                                   NTGSDQQAGLLVMTVDDGMKAGASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQ 1045
                                                                                                             SDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFR 985
                                                                                                                                                                                                                                              IDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVR 865
                                                                                                                                                                                                                                                                                                   NAL-DGNVFDS-----SAQGFATGA------TGLTDAIKNGVEGSINDF--
                                                                                                                                                                                                                                                                                                                                                                                                             GYHPKAQILSAWERIKALNPDIYFFGEGWDSNQS--DRFEIASQINLKGTGIGTFSDRLR 745
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   NSPENTVAYELTDHVN----
                                                                                                                                                                                     MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRI 925
                                                                                                                                                                                                                                                                                                                                      DSVRGGGPFDSGDALRONOGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVM 805
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                                                                                                                                                    MDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VLDDA-YAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVY-SADKKVI 338
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                                                                        RKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFL
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-KDKWGNIIVVYNPNKTVATINLPSGK-WAINATSG
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TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5731174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhicm F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1090RAMION: 7019 PARAY. (202) 429-0625
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
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          235
                                                                                                                     194 -TILWPGGODKPIVRLYYSHSSKVAADGEGKF-----TDRYLKLTPTTVSQQVSMRFP- 245
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CITY: Washington
STATE: D.C.
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  GGAHVTFSYIPSTHAVYDTINNPNAD--LQVESGVKTDLVTVTLGEDPDVSHTLSIQTDG
                                              ---HL-----SSYAAFKLPDNANVDELLQGET-----VAIAAAEDGILISATQVQTAG
                                                                                                                                                                TLGEGXSGFTVHDDTANKDIPVTSVKDASLGQDVTAVLAGTFQHIFG----GSDWAPDNH 185
                                                                                                                                                                                                        AFGD----FT--DRTVSVIAGNSAVYDSR------ADAFRAAFGVALAEAHWVDKN- 193
                                                                                                                                                                                                                                                   ----ADRYIDLSKGNEVWLVEGNSQIFYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPL 129
                                                                                                                                                                                                                                                                                           TPSGSDKY-----GPYWVIPLNKE------SGCINVIVRDGTDKLIDSDLRV 149
                                                                                   STLL-----KKVTNNLYQFSGDLP---EGNYQYKVALNDSW--NNPSYPSDNINLTVPA
                                                                                                                                                                                                                                                                                                                                  AGDYOPWSLWMWPKDGGGAEYDENQPADSFGAVASADIPGNPSQVGIIVRTQDWTKDVS-73
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   14.0%; Score 788.5; DB 1; 25.4%; Pred. No. 4.7e-58; tive 151; Mismatches 359;
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                                                                                                                                                                                                                           Sequence 11, Application US/08474545 Patent No. 5736375
                                                                                                                                                                                                          GENERAL INFORMATION:
                                                 APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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    STREET:
            ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, STREET: 2000 K Street, N.W., Suite 200
                                                                                                                                                                                                                                                                                                                                                     KVGESTLGQ-----AEGSVQVPGISMMIL 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQAKQVIPRNYLNSSQYYYSGDDL--GNTYTQKATTFKVWAPTSTQVNYLLYDSATGSVT
Washington
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REFERENCE/DOCKET NUMBER: 4121-43

TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEFX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.0%; Score 788.5; DB 1; Best Local Similarity 25.4%; Pred. No. 4.7e-58; Matches 282; Conservative 151; Mismatches 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MENTUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                             AL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVN
                             SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
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 INFORMATION
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DEWEER, PHILIPPE APPLICANT: AMORY, ANTOINE
                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1046 TAGENSLANGVQIAADGTVTLPAWSVAVL 1074
                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Wilhlem F. Gadiano
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                              STREET: 2000 K St
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                              APPLICATION NUMBER: US/0: FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                   TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
                                                                                            NAME: Wilhlem F. Gadiano, E REGISTRATION NUMBER: 37,136 REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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FOR SEQ ID NO:
                     650 383-5605
                                                                                                                                                                                                                                                                                                                                                                                                                     2000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                       WILLIAN BRINKS HOFER GILSON & LIONE, P.C 300 K Street, N.W., Suite 200
                                                                                                                                                                                                           US/08/478,341
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                                                                                              4121-45
                                                                                                                              Esq.
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 928 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186
866 MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRI 925
                                                                                                                                                              746 DSVRGGGPFDSGDALRQNQGTGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVM 805
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                                                                                                                                                                                                                                                                                                                634 WYYORLNETTGSVESATCCSDSAPEHRMFA-----KLIADSLAVWTTDYKIDGFRFDLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 TLGEGXSGFTVHDDTANKDIPVTSVKDASLGQDVTAVLAGTFQHIFG----GSDWAPDNH 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 AFGD----FT--DRTVSVIAGNSAVYDSR------ADAFRAAFGVALAEAHWVDKN- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 TPSGSDKY ----- GPYWVIPLNKE ------SGCINVIVRDGTDKLIDSDLRV 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VLDDA-YAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVY-SADKKVI 338
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                                                                          IDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVR 865
                                                                                                                     NAL-DGNVFDS-----SAQGFATGA------TGLTDAIKNGVEGSINDF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AADYSSKNLYLWN-----NETCDALSAPVA-----DW-NDVST 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPSGSDKY-----GPYWVIPLNKE-----SGCINVIVRDGTDKLIDSDLRV 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
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NTGSDQQAGLLVMTVDDGMKAGASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQ 1045
                                                         SDDGSNYEVITRYKEMVATPGEAELKOMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFR
                                                                                          MDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS
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                             ---RKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFL
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                               NEIHK-RGMGAILDVVYNH-----TAKVDLFEDLEPNYYHEM-DADGTPRTSFGGGRLG 122
                              TTHHMTKRLLIDSIKYLVDTYKVDGFRFDMMGDHDAASIEEAYKAARALNPNLIMLGEGW
                                                     PEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGW 716
                                                                                                                                 QAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSA 656
                                                                                                                                                                  -----ERLSDYASSNSNYNWGYDPQNYFSLTGMYSSDPKNPEKRIAEFKNLI
                                                                                                                                                                                                    QLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEG-TTRIKEFRTMI 596
                                                                                                                                                                                                                                      GVTHIQLLPVLSYYFVNELKNH---
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DSNQSDR----FEIASQINLKGTG-IGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGAGV 772
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(301) 10 NO: 72:
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25.2%;
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                                                                                                                                                                                                                                                                                                     ; Score 449.5; DB 4;
; Pred. No. 1.5e-29;
86; Mismatches 208;
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-476-519-2
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                                                                                                                                       NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
TELEFAX: (314)537-6047
                                                                                                                        TELEFAX: (314)537-604 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Barry, Gerar.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
APPLICANT: Krohn, Bradley M.
APPLICANT: No. 5750876el Isoamylase Gene, Compositions
APPLICANT OF INVENTION: Containing It and Methods of Using Isoamyla.
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 777 amino acids
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  911
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CITY: St.
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                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louis
                      protein
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Best Local Similarity
Matches 203; Conserv
                                    1019 VAINAAPESRTLNEFAGET------LQLSALQQTAGENSLANGVQIAADGTVTL 1066
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                                                                                                                                                                                                                                  PSDGGEDHNLSWNQGGIVAEQRKAARTGLALLMLSAGVPMITGGDEALRTQ------
                                                                                                                                                                                                                                                                                                                                                  MIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEAD....
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                                                                                                                LRKSSPLFTLGDGSAVMKRVD-FRNTGSDQQAGLLVMTVDDGMKAGA---SLDSRLDGLV 1018
                                                                                                                                                                                           GDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTE
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FGDSASAIYVAYNGWSGAVDFKLPWPGTGKQWYRVTDTATWNEGPNAV--ALPGSETL
                                                                           LRPANFYSASDTNGNVMEQLRWFKPDGAQ------ADSAYFNGADNHALAWRIDGSE 700
                                                                                                                                                        ---EG-----NNNTYNL-----DSAANWLYWSR--SALEADHETYTKRLIAFRKAHPA 649
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                                                                                                                                                                                                                                                                       ---LATRVRMQAVSLATVMLGQG1AFDQQGSELLRSKSFTRDSYDS
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RESULT 10
PCT-US95-09323-2
; Sequence 2, Application
; GENERAL INFORMATION:

PC/TUS9509323

TITLE OF INVENTION:

Novel Isoamylase Gene, Cor Containing It and Methods

Compositions ods of Using

Isoamylases

APPLICANT:

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Best Local Similarity
Matches 203; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 28-JUL-19
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 777 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               640
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   556
                                                                                                                                                                754
                                                                                                                                                                                                                                                                                                                                                           589 IKEFRIMIQAIKQDLGMNVIMDVVYNHINAAGP---IDRTSVLDKIV-----PWYYQRL
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                                                                                             805 MIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 KAAALAALGVTAVEFLPV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US OF FILING DATE: 28-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/09323
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                                                                                                                                                                                                                                                                                  AADA----TSVGSKPTRA-LKDEVIYEVHYRGLTRNDDSVPAAERGTY-----KGAAR
 PSDGGEDHNLSWNQGGIVAEQRKAARTGLALLMLSAGVPMITGGDEALRTQ--
                                                                                                                              FPAGWAEWNGLYRDALRKKQNKLGVETVTPGTLA---
                                                                                                                                                                                                                                                                                                                            TREWKAMVKAF-HDAGIKVYIDVVYNHTGEGGPWSGTDGLSVYNLLSFRGLDNPAYYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                 STVEEVLNQLKQSDSQD-NPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTR
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                                                                                                                                                                                             ---NSCQHGCFNFDKNDSGNALNR--IVAELPPRPAAGGAGADLIAEPWAIGGNSYQVGG
                                                                                                                                                                                                                             ERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLRD--SVRGG----GP
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                                                                                                                                                                                                                                                             SDYKYPWDNTGYGGNYNTRHPIAQNLIVDSLAYWRDALGYDGFRFDL-----ASYLG--
                                                                                                                                                                                                                                                                                                                                                                                             -----QETQNDQNDVDPNSTA------GDNY-WGYMTLNYFAPDRRYAYDKSAGGP 305
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ER READABLE FORM:
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                                                               -NDLYGDDGRKPWHSINFVVAHDGFTLNDLYAYNDKQNNQPWPYG
                              LATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDS
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ches 308;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Bonner, Grace I.
REGISTRATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
TITLE OF INVENTION: No. 5750876el
TITLE OF INVENTION: Containing It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                 352
370 TVYHPQSRKVEQYEVTDP-
                                                                                                                                                          299 AAEALSYGAQ--LADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTR-----DSASGA 351
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                                           59
                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                      2 AIDAQQLGARYDAAQANLAFRVYSSRATRVEVFLY---KNPTGSQEVARLALSKDPATQV 58
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 746 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                    WSLSLPTSTIKNTYGITGAVYYGYRAWGPNWPYDAAWTKGSATGFVSDVDNAGNRFNPNK 118
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o. 5750876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Grace L. Bonner, Monsanto Company, BB4F 700 Chesterfield Parkway No. 5750876th
                                                                                                                                                                                                 6.2%; Score 349; DB 1; Length 746; ilarity 22.4%; Pred. No. 7.2e-21; Conservative 101; Mismatches 304; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (314)537-6047
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YAHSLSTNSEYSQVVDLNDSALKPDGWDNLTM 419
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                                                                             ----WQGGS------DLKGAFYRYAM 369
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                                                                                                                                                                                                     Indels 284;
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PCT-US95-09323-11
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 28-JUL-1994
"INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application PC/TUS9509323 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Novel Isoamylase Gene, Compositions TITLE OF INVENTION: Containing It and Methods of Using: NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1029 TLNEFAGET-----LQLSATQQTAGENSLANGVQTAADGTVTL 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              680 AYNGWSGAVDFKLPWPGTGKQWYRVTDTATWNEGPNAV -- ALPGSETL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 LYRDALRKKONKLGVETVTPGTLA-----TR--FAGS------
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDGSAVMKRVD-FRNTGSDQQAGLLVMTVDDGMKAGA---SLDSRLDGLVVAINAAPESR 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NNTYNL-----DSAANWLYWSR--SALEADHETYTKRLIAFRKAHPALRPANFYSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- DALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKK
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; LENGTH: 746 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09323-11
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Best Local Similarity 22.4%;
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LENGTH: 746 amino acid
                                        1029 TLNEFAGET---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 TVYHPQSRKVEQYEVTDP------YAHSLSTNSEYSQVVDLNDSALKPDGWDNLTM 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AIDAQQLGARYDAAQANLAFRVYSSRATRVEVFLY---KNPTGSQEVARLALSKDPATQV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGSKPTRA-LKDEVIYEVHVRGLTRNDDSVPAAERGTY-----KGAARKAAALAALGV
                                                                                                                                                                                                                                                                                                                                                                                LYRDALRKKONKLGVETVTPGTLA-----TR--FAGS------
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AYNGWSGAVDFKLPWPGTGKQWYRVTDTATWNEGPNAV--ALPGSETL
                                                                                                                GDGSAVMKRVD-FRNTGSDQQAGLLVMTVDDGMKAGA---SLDSRLDGLVVAINAAPESR 1028
                                                                                                                                                       -NNNTYNL-----DSAANWLYWSR--SALEADHETYTKRLIAFRKAHPALRPANFYSAS
                                                                                                                                                                                         LQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTL
                                                                                                                                                                                                                               SWNQGGIVAEQRKAARTGLALLMLSAGVPMITGGDEALRTQ-----FG----
                                                                                                                                                                                                                                                           -----LATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNFDKNDSGNALNR--IVAELPPRPAAGGAGADLIAEPWAIGGNSYQVGGFPAGWAEWNG
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                                                                        DTNGNVMEQLRWFKPDGAQ------ADSAYFNGADNHALAWRIDGSEFGDSASAIYV
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                                    -----LQLSAIQQTAGENSLANGVQIAADGTVTL 1066
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PATENT OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE

PATENT NO. 5457037

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5457037-3
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APPLICATION NUMBER: 224,114
FILING DATE: 25-JUL-1988
SEQ ID NO:3:
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Best Local
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FILING DATE: 08-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 749,621
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       542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AAGITGAVY-YGYRAWGPNW------PYASNWGKGSQAGFVSDVDANGDRFNPN-- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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                                                                    YKASQEADLAT ---- RVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWF 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IHESHIRDLSAWDQTVPAELRGKYLALTAGDSNMVQHLKT--LSASGVTHVELL 485
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YSWDQGMSAGTGAAVNQRRAARTGMAFEMLSAGTPLMQGGDEYLRTLQCNNNAYNLDSSA 60:
                                                                                                                                            --DFSGSSNLFQSSGRSPWNSINFIDVHDGMTLKDVYSCNGANNSQAWPYGPSDGGTSTN
                                                                                                                                                                                                                EIDYNGAPGGYAA---DPTEVVNYVSKHDNQTLWDMIS-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVYMDVVYNHTAEGGTWTSSDPTTAT----IYSWRGLDNTTYYELTSGNQYFYDNTGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVIMDVVYNHTNAAG-----PTDRTSVLDKIVPW-----YYQRLNETTGSVESATCC 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QN-----YWGYMTENYFSPDRRYAYNKAAGGPTAEFQAMVQAF-HNAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVQE--TQNDANDVVPN------
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                                                                                                                                                                                                                                                                                            RDSLRQAQ-----NELGSMT------IYVTQDAN----
                                                                                                                                                                                                                                                                                                                                                                -DALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGS 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEGWDSNQSDRFEIASQINLK----GTGIGTFSDRLR----DSVRGGGPFDSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANFNTYNTVAQNLIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFF 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQKDDVIYEVHVRGFTEQDTSIPAQYRGTYYG--AG-----LKASYLASLGVTAVEFL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/1,797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Patent No. 5457037
;Patent No. 5457037
;APPLICANT: TOGNONI, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;
;GALLI, GIULIANO;LUCCHESE, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLO
; TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE
; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.9%; Score 334; DB 6; Best Local Similarity 22.5%; Pred. No. 1.4e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 08-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
462
                                                                            404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 SYGAQLADGGVTERVWAPTAQQVDVVVYSADKKVIGSHPMTRDSA-SGAW-----SWQG 356
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                                                                                                                                                                                                                                  289 KYYMDYYYNHTAEGGTWTSSDPTTAT----IYSWRGLDNTTYYELTSGNQYFYDNTGIG
                                                                                                                                                                                                                                                                                                                 246 QN-----YWGYMTENYFSPDRRYAYNKAAGGPTAEFQAMVQAF-HNAGI 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 GSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQV--VDLNDSALKPDGW 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 224,114 FILING DATE: 25-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 749,621 FILING DATE: 19-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                          NVIMDVVYNHTNAAG------PTDRTSVLDKIVPW-----YYQRLNETTGSVESATCC
                                                                                                                                                                                                                                                                                                                                      DNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAIKQDLGM 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQKDDVIYEVHVRGFTEQDTSIPAQYRGTYYG--AG-----LKASYLASLGVTAVEFL
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                                                                                                                GEGWDSNOSDRFEIASQINLK----GTGIGTFSDRLR----DSVRGGGPFDSG------
                                                                                                                                                                                                                                                                                                                                                                                                PVQE--TQNDANDVVPN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLLLDPYAQEVSQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLVPSTQSTGTKPTR 175
                                 -DALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGS 816
                                                                                                                                                     ANFNTYNTVAQNLIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYN 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGITGAVY-YGYRAWGPNW------PYASNWGKGSQAGFVSDVDANGDRFNPN-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176;
                                                                        FDAADSNVAIN-RILREFTVRPAAGGSGLDLFAEPWAIGGNSYQLGG-FPQGWSEWNGLF
                                                                                                                                                                                           SDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFF 712
                                                                                                                                                                                                                                                                                                                                                                                                                                      PVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQ 545
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	234 ATNGF-ISAVREFKMMVRAL-HAAGFEVIVDVVYNHTGEGGVLGPTLSERGIDNRAYY 309	
	580 ATDPEGTTRIKEFRIMIQAIKQDLGMNVIMDVVVNHTNAAGPTDRTSVLDKIVPW	
	Db 228	
	Qy 520 SEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSY 579	
	Db 199 LTCEPVLEHLKQLGVTTIQLLPVHAKVHD 227	
	QY 460 LTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQFFSRLCEVNSAVKS 519	
	Oy 409 -LKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYLA 459	
	: 	
	QY 369 MTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSA 408	
	27	
	KKVIGSHPMTRDSASG-AWSWOGGSDIKGAFYRYA 36	
32;	Query Match 5.7%; Score 319.5; DB 3; Length 726; Best Local Similarity 22.2%; Pred. No. 2.2e-18; Matches 160; Conservative 88; Mismatches 219; Indels 253; Gaps	
	; UKGANISM: Knodothermus marinus US-09-129-075-4	
	20	
	SEQ ID NO	
	NUMBER OF SEQ ID NOS: 16	
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	APPLICANT: Bisgard-Frantzen, APPLICANT: Svendsen, Allan	
	APPLICANT:	
	Patent No. 6087149 GENERAL INFORMATION:	
	RESULT 15 US-09-129-075-4 : Secuence A Application US/00120075	
	Db 630 HP 631	
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	OY 907 NRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKS 966	
	Db 543 YSWDOGMSAGTGAAVDORRAARTGMAFEMLSAGTPLMQGGDEYLRTLQCNNNAYNLDSSA 602	
	OY 852 YKASQEADLATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWF 906	
	Db 485 DFSGSSNLFQSSGRSPWNSINFIDVHDGMTLKDVYSCNGANNSQAWPYGPSDGGTSTN 542	
	QY 817 EIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMIS	

B	Q	В	Qy	DЬ	οy	ф	Qy	Db	Qy	g B	Qy
541	888	481	855	448	796	412	741	364	690	310	637
541 ELSRTQHGNNNAYCQDNEISWYNWQLDTRKQQFLEFVRQTIWFRKQHRSFRRRHFLTGLP 600	ELLRSKSFTRDSYDSGD	481 HNEANLEGNRDGMDENYSTNCGVEGPTQDPSVLACREALKRSLISTLELSQGVPMLLGGD 540	855 SQEADLATRVRMQAVSLATVMLGQGIAFDQQGS 887		796 MAGNLADFVMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNOTLWDMISY-KA 854	412 QWTEWNGRYRDAVRREWRGDRGLNGEFATREAGSSD 447	~	364 LARELYDVDMLSTFFQVIQQDPVLSQVKLIAEPWDVGPGGYQVGHFPW 411	690 HPKAQILSAWERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTF 740	310 KADPNNPRELVDYTGTGNTLDVGNPYVIQLIMDSLRYWVTEMHVDGFREDLAAA 363	637 ORLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGY 689
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Search completed: April 22, 2001, 09:05:59 Job time: 4043 sec

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April 22, 2001, 09:04:38; Search time 62.87 Seconds (without alignments) 1192.568 Million cell updates/sec

Title: Perfect score:

US-09-262-126C-4 5633 1 MLRYTRNALVLGSL

Sequence: MLRYTRNALVLGSLVLLSGC..... .AVLELPQGEAQGAGLPVSSK 1091

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum Maximum DB DB seq length: length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

<u>*</u> 3 : 1 PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) precursor - Klebsiell N;Alternate names: pullulanase C;Specites: Klebsiella pneumoniae C;Date: 13-Jan-1995 **sequence_revision 13-Jan-1995 **text_change 08-Oct-1999 C;Accession: S1183; A33880 R:Kornacker, M.G.: Pugsley, A.P. Mol. Microbiol. 4, 73-85, 1990 Klebsiella pneumon

A; Title: Molecular characterization of pulA and its A; Reference number: S11823; MUID:90205629 A; Accession: S11823

product, pullulanase,

a secreted

A; Status: preliminary

A; Molecule type: DNA
A; Residues: 1-1090 < KOR>
A; Cross-references: EMBL: X52181; NID: g43912; PIDN: CAA36431.1; PID: g43913
A; Cross-references: EMBL: X52181; NID: g43912; PIDN: CAA36431.1; PID: g43913
R; D'Enfert, C.; Pugsley, A.P.
J. Bacteriol. 171, 3673-3679, 1989
J. Bacteriol. 171, 3673-3679, 1989

A;Title: Klebsiella pneumoniae pulS gene encodes an outer membrane lipoprotein requir A;Reference number: A32880; MUID:89291709
A;Accession: A32880

A; Status: preliminary

A; Molecule type: DNA A; Residues: 944-1090 <DEN>

A;Cross-references: GB:M29097; NID:9342046; PIDN:AAA61976.1; PID:9643577 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

рь δð QΥ . B Qy 망 QY 망 Qγ Query Match Best Local S Matches 1090; 181 180 120 121 60 61 Local Similarity SMREPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQTAGVLDDAYAEAA 300 QAVIHLVDIAGITSSSAADYSSKNLYLMNNETCDALSAPVADMNDVSTTPSGSDKYGPYW 120 VIPLNKESGCINVIVRDGTDKLIDSDLRVAFGDFTDRTVSVIAGNSAVYDSRADAFRAAF 180 VIPLNKESGCINVIVRDGTDKLIDSDLRVAFGDFTDRTVSVIAGNSAVYDSRADAFRAAF Conservative 99.78; Score 5618.5; Pred. No. 0; 0; Mismatches 0 DB 0 2 Indels Length 1090; -Gaps 240 179 239 :

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RESULT 2
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A16879
Alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1
Alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1
N.Alternate names: pullulan 6-glucanohydrolase; pu
C;Species: Klebsicila pneumoniae
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988
C;Accession: A26879; 802472
R;Katsuragi, N.; Takizawa, N.; Murooka, Y.
J. Bacteriol. 169, 2301-2306, 1987
A;Title: Entire nucleotide sequence of the pullulan
A;Reference number: A26879; MUID:87194626
A;Note: K. aerogenes
A;Accession: A26879
A;Molecule type: DNA
A;Residucs: 1-1096 <KAT>
A;Experimental source: strain W70
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IGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGSEIDYNGAPG
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A; Molecule type: DNA
A; Residues: 1-74 <CHA>
A; Residues: 1-76 <CHA>
C; Genetics:
A; Genetics:
A; Gene: pulA
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C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted <STG>
F;20-1096/Product: alpha-dextrin endo-1,6-alpha-glucosidase #status
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A;Title: Collagen-like sequences: A;Reference number: S02472; MUID:
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A; Status: not compar
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            NPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLRDSVRGGGFFDSGDALRQNQG
                                                  VESATCCSDSAPEHRWFAKLIADSLAVWTTDYKIDGFRPDLMGYHPKAQILSAWERIKAL
                                                                  VESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSÅWERIKAL
                                                                                                         TARIKEFRIMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGS
                                                                                                                      TTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGS
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R;Janse, B.J.H.; Steyn, A.J.C.; Pretorius, I.S.
Curr. Genet. 24, 400-407, 1993
A:Title: Regional sequence homologies in starch-degrading enz
A;Reference number: S38801; MUID:94130317
A;Accession: S38801
A;Molecule type: DNA
A;Residues: 1-1038 < JANN
A;Cross-references: EMBL:L19312
A;Experimental source: ATCC 15050
A;Cross-references: EMBL:L19312
A;Experimental source: ATCC 15050
B;Chapon, C.; Raibaud, O.
J. Bacteriol. 164, 639-645, 1985
A;Title: Structure of two divergent promoters located in fron A;Reference number: A91807; MUID:86033621
A;Accession: A25025
A;Molecule type: DNA
A;Residues: 1-65 < CHAN
A;Residues: 1-65 < C
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S3801
alpha-dextrin endo-1,6-alpha-glucosidase
N;Alternate names: pullulanase
C;Species: Klebsiella pneumoniae
A;Variety: ATCC 15050; strain K21
C;Date: 07-Apr-1994 #sequence_revision 07
C;Accession: S3801; A25025; S04864
                                                                                                                                                                                                                                                                             A;Title: Klebsiella pneumoniae strain K21:
A;Reference number: S04864; MUID:89343636
A;Accession: S04864
A;Molecule type: protein
A;Residues: 'X',21-31,'X',33,'X' <KOR>
A;Experimental source: strain K21
C;Genetics:
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C;Keywords: glycosidase; hydrolase; lipoprotein; polysacc
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1038/Product: pullulanase #status experimental <MAT>
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C;Date: 07-May-1995 #
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C;Accession: S51324
R;Kenz, A.; Schmid, R.; Kossmann, J.; Beck, E.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence of a cDNA of the Spinacia oleracea L. starch debranching enzyme.
A;Reference number: S51324
A;Accession: S51324
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-964 <REN>
A;Cross-references: EMBL:X83969; NID:g634092; PID:g634093
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   GMPRISDDGSNYEVITRVKEMVATPG-EAELKQMTAFYQELT---ELRKSSPLFTLGDGS
                                                    ATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNV
                                                                                                                                                                                                                                                                                                                                                                       LQLPGVIDELY-----SYDGPLGAVFSENTISLYLWAPTAQAVSASIF----KDPSGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALAEAHWVDKNTLLW----PGGQDKPIVRLYYSHSSKVAADGEGKFTDR-----YLKL 231
                                    DERCRYNHLATSILALSQGIPFFHAGDELLRSKSLDRDSYNSGDWFNRLDFSYNSNNWGV
                                                                                                  DYILTNCDGKQVKGSEVYTYGGTPVGYAMQPIETINYVSAHDNETLFDIVSLKTPTYITV
                                                                                                                                   DFVMIDKDGAAKKGSEI-DYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADL
                                                                                                                                                                   DAVLGGGPF--GPPLQ--QGYVTGLSLQPNDHDHSGKANADRMLAVAKDHIQVGMAGNLR
                                                                                                                                                                                                    DSVRGGGPFDSGDALRQNQGIGSGAGVLPNE---LASLSDDQVRHLA-DLTRLGMAGNLA
                                                                                                                                                                                                                                       KATNMLQGLSKNIDGVEGSSIYLYGEGWDFGEVANNARGVNASQLNLGGTGIGSFNDRIR
                                                                                                                                                                                                                                                         SAWERIKALNPD-----IYFFGEGWDSNQ---SDRFEIASQINLKGTGIGTFSDRLR
                                                                                                                                                                                                                                                                                                          LR-RDNDGATENSTCVNDTASEHFMVERLILDDLKHWAVNYKVDGFRFDLMGHIMKHTMV
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| : |::|::|::|| :| : :| :| | | | :| ::|
                                                                                                                                                                                                                                                                                                                                                                                                           GSYATDPEGTTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYY
                                                                                                                                                                                                                                                                                                                                                                                                                                            *KKWKF*****VDTKRFETLPPDSEEQQAQITAIRDEDGYNWGYNPVLWGTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLAFTSQDSAGVNHLEKLSAAGLTHVHLLPSFQFAEVDD--DK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLLADLSSETLKPEGWENLADEKPHLLSP----SDISLYELHIRDFSAYDLTVHPDLRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQVVDLNDSALKPDGWDNLT---MPHAQKTKADLAKMTIHESH1RDLSAWDQTVPAELRGK 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLOTVOLIESNGVWSAVGPRTWEGCYYVYEITVYHHSTLRIEKSFAIDPYARGISADVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMTR---DSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEY 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQTAGVLDDAYAEAAEALSY----GAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSCRAYWPSKYTFAWNVDIGNGS-----YYLFASKTAA---LKFTDAGIEGYDVKIKL
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Pred. No. 4.2e-83;
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starch debranching enzyme, pullulanase-type - maize
C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Oct-1999
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Oct-1999
C;Accession: T01688
R;Beatty, M.K.; Rahman, A.; Cao, H.; Woodman, W.; Lee, M.; Myers, A.M.; James, M.G.
Plant Physiol: 119, 255-266, 1999
A;Title: Purification and molecular genetic characterization of ZPU1, a pullulanase-t
A;Reference number: Z14395; MUID:99097061
A;Reference number: Z14395; MUID:99097061
A;Recession: T01688
A;Status; preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-962 <BEA>
A;Cross-references: EMBL:AF080567; NID:93411265; PIDN:AAD11599.1; PID:93411266
A;Experimental source: endosperm
C;Genetics:
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C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGYLDDAYAEAAEALSYGAQLADGGYTFRVWAPTAQQVDVVVYSADKKVIGSHPMTR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLTPTT--VSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVAVAESAQGFLLDARAYWVTKSLIAWNISDQKTSLFLYASRNATMCMSSQDMKGYDSKV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVALAE-----AHWVDKNTLLWPGGQDKPIVRLYYSHSSKVAADGEG-KFTDRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPPKDHNESNWPLI---KKRLANPSYKPDKNHITAAVENFTNLLQIRYSSPLFRLRSAK
                                                                                                                                                                                                                                                                                                                                     LNDSALKPDGWDNLTMPHAQKTKAD-LAKMTIHESHIRDLSAWDQTVPAELRGKYLALTA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPGVLDDMFAYTG----PLGTIFSEEAVSMYLWAPTAQDVSVSFYDGP-----AGPLLETV
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                  ETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWE
                                                                                                TDPEGTTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLN
                                                                                                                                                                                                                                   QDSVGIEHLKKLSDAGLTHVHLLPSFQFGGVDD------IKS---
                                                                                                                                                                                                                                                                                                               QLNELNGVWSVTGPRNWENRYYLYEVTVYHQTTGNIEKCLAADPYARGLSANSTRTWLVD
                                                                                                                                                                                                                                                                                                                                                                                                                     --DSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELQPENDGLPSSVTQKFPFISSYRAFRIPSSVDVATLVKCQLAVASFDAHGNRQDVTGLQ
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DSNGQTENSAAVNNTASEHFMYDRLIVDDLLNWAVNYKVDGFRFDLMGHIMKKTMIRAKS
                                                                       SNPDGPSRIIEYRLMVQALNR-LGLRVVMDVVYNHLYSSGPFAITSVLDKIVPGYYLR-R
                                                                                                                                                     ----NWKCVDEIELSKLPPGSDLQ-----QAAIVAIQEEDPYNWGYNPVVWGVPKGSYA
                                                                                                                                                                                          AGYCDSGSTVEEV-LNQLKQ-SDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYA
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Mismatches 3
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A; Residues: 1-904 <LOK>
A; Cross-references: EMBL:AF022725; NID:g2502057; PIDN:AAD04189.1; PID:g2677837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: Isolation and characterization of starch debranching enzyme, limit dextra A;Reference number: z15320
A;Accession: T04377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision
C:Accession: T04377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) - barley N;Alternate names: pullulanase (Species: Hordeum vulgare (barley)
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A;Introns: 21/3; 70/1; 87/3; 124/1; 169/3; 235/2; 285/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated
                                                                                                                                                                                                                                                                         Query Match 25.3
Best Local Similarity 35.7
Matches 330; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKALNPD------IYEFGEGWDSN---QSDRFEIASQINLKGTGIGTFSDRLRDSVR 749
                                                                                                                                                          QVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQTAGVLDDAYAE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLSAIQQTAGENSLANGVQIAADGTVTLPAWSVAVLELPQ 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGPFDSGDALRONOGIGSGAGVLPNELASLSDDQVR----HLADLTRLGMAGNLADFVM
                                                                                                                                                                                                      ARAYWVTSDLIAWNVGELEAQSVCLYASRAAAMSLSPSNGGIQGYDSKVELQPESAGLPE 86
                                                                                                                                                                                                                                        AEAHWVDKNTLLWPGGQ-DKPIVRLYYSHSSKVA---ADGEGKFTDRYLKLTPTT--VSQ 238
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EWENRYYLYEVDVYHPTKAQVLKCLAGDPYARSLSANGARTWLVDINNETLKPASWDELA
                              DLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDNLT 418
                                                                                                  AAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGAWSWQGGS 358
                                                                                                                                      TVTQKFPFISSYRAFKVPSSVDVASLVKCQLVVASFGADGKHVDVTGLQLPGVLDDMFAY 146
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                                                                  TG---PLGAVFSEDSVSLHLWAPTAQGVSVCFFDGPAGPALETVQLKES-NGVWSVTGPR 202
                                                                                                                                                                                                                                                                                                                                                             glycosidase; hydrolase
                                                                                                                                                                                                                                                                         25.3%; Score 1424.5; DB 35.7%; Pred. No. 2.2e-78; tive 176; Mismatches 341
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A;Residues: 1-910 \n...
A;Cross-references: GB:AE001900;
A;Cross-references: GB:AE001900;
                                                A; Molecule type: DNA
A; Residues: 1-910 <WHI>
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T.; Zalewski,
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nes 345; Conservative
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                                                                                   --LSGGVSATNPYRDLLVIFNGSADAVTLNDASASGMKLHPVLAASSDPIVRTSKVSGTQ
                                                                                                         DGMKAGASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQTAGE----NSLANGVQ
                                                                                                                                                           VATPGEAELKOMTAFYOELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDOOAGLLVMTVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVIVEDGTDKLIDSDLRVAFGDFT----DRTVSVIAGNSAVYDSRADAFRAAFG------ 181
                                                                                                                                    KVTP--ADITRASDHFRELLRVRSSSSLFRLDTAAQVQQSLSF----LPAPTGVIAMK--
                                                                                                                                                                                                          QGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSN---YEVITRVKEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVSMRFPHLSSYAAFKL--PDNANVDELLQGETVATAAAEDGILISATQVQTAGVLDDAY 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VALAEAHWVDKNTLLWPGGQDKPIVRLYYSHSS--KVAADGEGKFTDRYLKLTPTTVSQ 238
                                    *ASVPALTTAV
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157; Mismatches 365;
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T03760

alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) - rice

N;Alternate names: pullulanase

C;Species: Oryza sativa (rice)

C;Date: 23-Apr 1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000

C;Accession: T03760

C;Acces
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A;Accession: T03760
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-986 < NAK>
A;Cross-references: EMBL:D50602; NID:9836661; PIDN:BAA09167.1; PID:91783306
A;Cross-references: EMBL:D50602; NID:9836661; PIDN:BAA09167.1; PID:91783306
A;Experimental source: cv. Fujihikari, endosperm
C;Genetics:
A:Map position: 4
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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Best Local Similarity
Matches 333; Conserv
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                                                                                                                                                                                                                                                                                                                                                                         IADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPD------IYFFGEGWD
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                                                                                                                                                                                                             SN---QSDRFETASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPMTR-----DSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNS
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                                              NELASLSDDQVRH----LADLTRLGMAGNLADFVMIDKDGAAKKGSEI-DYNGAPGGYAA
                                                                                                                                                                                                                                                                                                                          TVDDLLNWAINYKVDGFRFDLMGHIMKSTMIRAKSAIRSLTRDVHGVYGSKIYLYGEGWD
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NGYYQGNEADTRRELATYADHIQIGLAGNLKDYVLRTHTGEAKKGSDIYTFDGSPVGYTS
                                                                                                                                                               FGEVAQNKRGINASQINMSGTGIGSFNDRIRDSVNGGNPF--GNPLQ--QGFSTGLFLEP
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33.8%; Pred. No. 2.2e
tive 160; Mismatches
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1.2e-72;
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C;Accession: H72204
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hiv
R;Nelson, K.E.; Clayton, R.A.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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A;Residues: 1-843 <ARN>
A;Residues: 1-843 <ARN>
A;Cross-references: GB:AE001821; GB:AE000512; NID:g4982421; PIDN:AAD36907.1;
A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pullulanase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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KPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYLAL----TAGDS 465
                                                                                                                                                                                                                                                                                                                                                                                                                                             YWVIPLNKESGCINVIVR----DGTDKLIDSDLRVAFGDFTDRTVSVIAGNSAVYDSRAD 174
                                                                                                                                                                                            AYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRD-SASGAWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPVETINYVSAHDNETLFDIVSIKTPIGLSIDGECRINHLASSMIALSQGIPFFHAGDEI 792
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                                                                                                                                                                                                                                        DID-----VTNYVRIVLSESLKEEDLRKDVELIIEGYKPARVIMME-----ILDD
                                                                                                                                                                                                                                                                              TVSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQTAGVLDD 294
                                                                                                                                                                                                                                                                                                                                                                  AFRAAFGVALAEAHWVDKNTLLWPGGQDKPIVRLYYSHSSKVAADGEGKFTDRYLKLTPT
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                                                                  AVVEGDLDGVFYLY-----QLENYGKIRTTVDPYSKAVYANSKKSAVVNL--ART
                                                                                                          WQGGSDLKGAFYRYAMTVYHPQSRKVEQY----EVTDPYAHSLSTNSEYSQVVDLNDSAL
                                                                                                                                                                                                                                                                                                                          TSPRIF-FAQARSNKVIEAFLTNPVDTKK-----KELFKVTVDGKEIPVSRVEKADPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETTIVVHYHRYDG-----KYDGWNLWIWPVE-----PVSQ-EGKAYQFTGEDDFGK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENQAVIHLVDIAGITSSSAADYSSKNLYLWNNETCDALSAPVADWNDVSTTPSGSDKYGP 118
                                                                                                                                                    YYYDG----ELGAVYSPEKTIFRVWSPVSKWVKVLLFKNGEDTEPYQVVNMEYKGNGVWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.5%; Score 703.5; DB 2; 24.9%; Pred. No. 1.1e-34; tive 150; Mismatches 386;
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	819 GTEVIETVEGTIELDPLSAYVL 840	В
	1055 GVQIAADGTVTLPAWSVAVL 1074	Οy
818	776 MLKDHAGGDPWKD-IVVIYNGNLEKTTYKLPEGKWNVVVNSQKA	Db
1054	NEFAGETLQLSAIQQTAGENSLAN	Qy
775	727RKLQFIDVFNYHKGLIKLRKEHPAFRLKNAEEIKKHLEELPGGRRIVAF 775	DЪ
994	.935 ITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAG	Qy
726	689 LTSQGVPELHGGQDFCRTKNFNDNSYNAPISINGFDYE-	Db
934	877GQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEV 934	Qy
688	629 YDGKLIKSFALDPEETINYAACHDNHTLMDKNYLAAKADKKKEWTEEELKNAOKLAGAIL	DЬ
876	820 YNG-APGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVRWQAVSLATVWL 876	Qy
628		Db
819	764 QGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGSEID	Qy
598	555 IDPTILYGEPWGGWGAPIRFGKSDVAGTHVAAFNDEFRDAIRG	Db
763	705 LNPDIYFFGEGWDS-NQSDRFEIASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQN 763	Qy
554	495 YLNESGCGNVIASERPMARKFIVDTVTYWVKEYHIDGFRFDQMGLIDKKTMLEVERALHK	Db
704	645 SVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGEREDLMGYHPKAQILSAWERIKA 704	Qy
494	439 PHTRIREVKEMVKALHKH-GIGVIMDMVFPHTYGIGELSAFDQTVPYYFYRIDKTGA	DЬ
644	586 T-TRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETIG 644	Qy
438	416YNWGYDPYLFWYPEGRYSTDFKN	Db
585	526 CDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEG 585	Qy
415	378 GVTTGLSHLVELGVTHVHILPFFDFYTGDEL-DK	Дb
525	466 NMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGY 525	Qy
377	323 NPEGWENDRGPKIEGYEDAIIYEIHIADITGLENS-GVKNKGLYLGLTEENTKGPG 377	Db

RESULT 10

G69585

G191ulanase amyX - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Cpate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: G69585
R;Knnst, F; Ogasawara, N.; Moszer, T.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudegg, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rleger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasamoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Residues: 1-718 «KUN>
A;Rosidues: 1-718 «KUN>

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A;Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14971.1; A:Experimental source: strain 168
C;GenetLcs:
A;Gene: amyX
RESULT 11
A84112
AB4112
Alkaline amylopullulanase BH3697 [imported] -
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-
C;Accession: A84112
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                                                                                                                                                                                                                                978 VMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSRLD-----GLVVAINAAPES----
                                                                                                                                                                                                                                                                                                    918 YNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRTAAFDDEFYYDG----ELGAVYTADHTVFKVWAPAATSAAVKL-----SHPNKS
                                                                                                                                                                                                                                                                                                                                                          ADLATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNN
                                                                                                                                                                                                                                                                                                                                                                                                       KALAPIV------PEPSQSINYVESHDNHTFWDKMSFALPQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEKTVPGYFFRHDECGMPSNGTGVGNDIASERRMARKFIADCVVYWLEEYNVDGFRFDLL
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                                                                                                                                                                                                                                                                                                                                     NDSRKRSR-QRLAVAIILLAQGVPFIHSGQEFFRTKQGVENSYQSSDSINQLDWDRRET-
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                                                                                                                                                                 RTLNEFAGETLQLSAIQQTAGENSLANGVQIAADGTVTL 1066
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                                                                                                                                                                                                                                                                     ·----FKEDVHYIRRLISLRKAHPAFRL----
               01-Dec-2000 #text_change
                                                Bacillus halodurans (strain C-125)
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R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halod A; Reference number: A83850; MUID:20263314

A:Accession: A84112

A:Status: preliminary
A:Status: preliminary
A:Residues: 1-1072 <STO>
A:Cross references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07416.1; A:Experimental source: strain C-125
C:GenetLcs:
A:Gene: BH3697
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Best Local Similarity 23.3
Matches 262; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 GLDPYAKSMAAWNNEGSYSI------GKAAIVDPSSIGPELDFAEIEGFEKREDAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAENIGFLVL-----NTATGDKDGND-KHVQLLSPEM----KEIWIKEGSDDVFL 140
 QINLKGT-GIGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRH 787
                                        WVEEYKVDGFRFDMMGDHDAETIQIAYDRAKELNPNIVMIGEGWRTYVGDEHGGDIMPAD
                                                                        WTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDSNQSDR----FEIAS
                                                                                                             YNHTAA-----VEIFEDLMPNYYHFM-DADGTPRTSFGGGRLGTTHKMSRRILVDSITY
                                                                                                                                              YNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAV
                                                                                                                                                                                                      NTLVAQTDSYNWGYDPFHYTVPEGSYATDPEG-TTRIKEFRTMIQAIKQDLGMNVIMDVV
                                                                                                                                                                                                                                                                                                                                               YRIIKDDIDMTKGD-QGVWQVTLHSENTGLDNLAGYYYHY
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                                                                                                                                                                                 -----NNYNWGYDPHSYFSLSGMYSENPEDPELRIKEFKHLIDEIHR-RGMGVILDVV
                                                                                                                                                                                                                                                                                       NEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQAL 553
                                                                                                                                                                                                                                                                                                                            IYEVHVRDFTS-DPGIEEELTAQFGTF----ASFVDKLDYIEDLGVTHIQLLPVMSY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VIGSHPMTRDSASGAWSW-----QGGSDLKGAFYRYAMTVYHPQSRKVEQYEVT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LISATOVOTAG--VLDDAYAEAAEALSYGAOL-ADGGVTFRVWAPTAOOVDVVVYSADKK
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                                                                                                                                                                                                                                                      -YWGDELANHERELA------YSSSG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GDDTVYTNPYYQTIEGLVSGELISLTEMELRFTS
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QDWMQHTESVGVFSDEFRNELK

SEGQPRF

753

Qy 460 LTAGDSNMYQHLKTLSASGVTHVELLPVEDLATVNEFSDKVADIQQPFSRLCE 512	Qy 280 LISATQVQTAGVLDDAYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIG 339	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-717 <sto> A; Coss-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06983.1; GSPDB:GN00 A; Cross-references: GB:AP001518; C-125 C; Genetics: A; Gene: amyX Query Match Best Local Similarity 26.1%; Pred. No. 3.9e-28; Matches 203; Conservative 99; Mismatches 290; Indels 187; Gaps 28;</sto>	RESULT 12 H84057 H84057 pullulanase amyX [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000 C;Accession: H84057 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: H84057 A;Status: oreliminary A;Status: oreliminary	OY 984FRNTGSDQQAGLLVMTVDDGMKAGASL-DSRLDGLVV 1019	Qy 895	Oy 788 LADLTRLGMAGNLADFVMIDKDGAAKKGSEIDYNGADGGY-AADPTEVVNYVSKHDNQ 844 Db 754 IT
Db 81 GYRVHGPYEPDAGHRENNKLLLDPYAKQLVGRLRWSEALFGYTIGSADADLSFDERD- 138 81 GYRVHGPYEPDAGHRENPNKLLLDPYAKQLVGRLRWSEALFGYTIGSADADLSFDERD- 138 Qy 418 TMPHAQKTKA-DLA	Superfam Superfam Query Ma Best Loc Matches Matches 25	.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A; Reference number: AB2950; MUID:20437337 A; Accession: CB3375 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-716 < CSTO> A; Cross-references: GB:AE004643; GB:AE004091; NID:g9948178; PIDN:AAG05548.1; GSPDB:GN A; Experimental source: strain PA01 C; Genetics: A:Genetics:	Qy 975 GSAVMKRYDERNTGSDQQAGLLVMTYDDGMKAGASLDSRLDGLVVAIN 1022	Oy 921 GMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGD 974	QY 806 IDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVR 865	Oy 692 KAQILSAMERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLR 745

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probable glgX protein - Mycobacterium tuberculosis (strain H37RV)

C;Specles: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: A70764

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A;Auture 393, 537-544, 1998

A;Auture 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Feference number: A70500; MUID:98295987

A;Accession: A70500; MUID:98295987

A;Accession: A70500; MUID:98295987

A;Cross-references: GB:Z74020; GB:AL123456; NID:g3261584; PIDN:CAA98327.1; PID:g1403478
A;Experlmental source: strain H37Rv
C;Genetics:
A;Gene: glgX
C;Superfamily: glyX protein
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                                                                                 Query Match 6.3
Best Local Similarity 22.8
Matches 197; Conservative
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--ASGQVNEFKEMV-AHLHDAGLELILDVYYNHTAEGNELGPTLCMRGIDNASYY-RLMP
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                                          ALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGAWSWQGGSDLK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLLDGRAQPTGILRSGEDATLLLILNAYHDAVSFRLPEVAEGSGWTCLLDTQRPEDPLGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAFTQRLLALRQRYPILRRGRFLVGEYNEALGVKDVTWLAPGGEEMTEEHWHDEHARCLG
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                                                                                 6.3%; Score 352.5; DB 2; Length 22.8%; Pred. No. 1.7e-13; ative 113; Mismatches 294; Indels
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glycogen operon protein Glgx - Deinococcus radiodurans (strain R1)
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Date: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C.Accession: B75540
R.White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Venathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu A; Reference number: A75250; MUID:20036896
A;Accession: B75540
A;Residues: 1-720 <WHI>
                                                                                                                                                                                                                                                                                                                                                                  RESULT
B75540
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T.; Zalewski,
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A;Cross references: GB:AE001888; GB:AE000513; NID:g6457936; PIDN:AAF09848.1; PID:g645793 A;Experimental source: strain R1 C;Genetics: A;Gene: DR0264 A:Map position: 1 C;Superfamily: glyX protein 밁 Qy 밁 Qy В Ş δÃ 밁 δÃ В δÃ В δõ В Ş 밁 Qy 밁 20 밁 Ş 밁 Ş 밁 Ş 밁 Š õ В Š 밁 Query Match Best Local Similarity Matches 198; 1083 GAGLPVSS 1090 1025 PESRTLNEFAGETLOLSATOQTAGENSLANGVOTAADGTVTLPAWSVAV--LELPOGEAO 1082 978 VMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSR-----LDGLVVAINAA------ 1024 557 939 KEMVATPGEAELKQMTAFYQELTELRKSSP-----LFTLG--------DGSA 977 525 879 GIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRV 938 847 WDMISY----KASQEAD------LATRYRMQAYS--LATYMLGQ 878 437 787 HLADLTRIGMAGNIADFYMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTL 846 734 GTGIGTF-----SDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVR 786 349 FREDLASTLARGLHEVDQ-LSGFFTIIHQDPIISQVKLIAEPWDVGEG------ 395 629 DKIVPWYYQRLNET-----TGSVESATCCSDSAPEHRWFAKLIADSLAVWTTDYKIDG 681 219 ------LLDKGLT-----517 VKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPE 576 185 YAGVAT--PAILDYLRDL---GITAIEFLPVHQ------HVDDPF------457 YLALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSA 516 417 LTMPHAQKTKADLA-------KMTIHESHIRDLSAWDQTVPAELRGK 456 362 GAFYRYAMTV---YHPQS--RKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDN 416 306 GAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSH----PMTRDSASGAWSWQGGSDLK 361 465 RDSVTYEOKHNEANGEGNNDGHNHNITWNCGVEGPTDDPEINRLRGOOMRNFLATLLLGO 524 396 GYQVGNFPVNWAEWNGIYRDDMR------SFWKGEGGLASEIGY----RIT 436 682 FRFDL-----MGYHPKAQILSAWERIKALNP---DIYFFGEGWDSNQSDRFEIASQINLK 733 297 DN--PTYYRLVADDQRFYFDYTGTGNSLNV-----RHPQTLQLIMDSLRYWVTEMHVDG 348 69 QPGQRYGYRVHGEYAPEKGLRFNPNVVLLDPYAKALDGTEQFDRGV----FGYVAGGEDD 124 17 GATWDGKGTNFALYSENATGVELCLFDAE-----GHETRFPLTEQT---AFVWHGYLPGI 68 SQMQEEEQRGAPLGLVVDPMFNWVGDQKPGIPFHQSVIYEAHVKGLTMTHPDVPEELRGT 184 PDLGGCGEW----DLLLDTSDDGAEE------KVAAGGETTLRGRSVKLYRCQVPEKELE 712 EMSDEDWNN---PQTQSLGMFLAGDGL---ADVDAEGKPLTDDHLLLLLSSSYVDLPFKM 662 ------WEKVDEELLAFTRKLIALRKAHPSLHRRKFFAGRNIRGEDVRDIVWLRFDG-A 608 6.1%; Score 344.5; DB 2; Length 720; illarity 21.8%; Pred. No. 5e-13; Conservative 113; Mismatches 270; Indels 327; Gaps ----NY-WGYSTLNFFAPD 239 218 45;

Db 713 KLAEPAEA 720

Search completed: April 22, 2001, 09:04:57 Job time: 4138 sec

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Run on:
                                                                                                             OM protein - protein search, using sw model
April 22, 2001, 09:11:53; Search time 52.01 Seconds (without alignments) 718.568 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Title: Perfect score: Sequence:

US-09-262-126C-4
5633
1 MLRYTRNALVLGSLVLLSGC.....AVLELPQGEAQGAGLPVSSK 1091

Scoring table:

Searched: 93435 seqs, 34255486 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

93435

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

33332222222222211111111111111111111111	Result
703.5 703.5 703.5 352.5 352.5 334 302.5 167.5 166.5 166.5 158.5 158.5 158.5 149.	Score
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AMY_STRLI	GLGB_BUTFI	P3P_LACLC	GLGB_SOLTU	AMYR_BACS8	GLGB_BACST	CDAS_BACSH	GLGB_SYNP7	POLG_EMCVD	POLG_EMCVB	AMY_BACME	AMY3_DICTH
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ALIGNMENTS

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Pred. No. 0;
0; Mismatches
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N-ACYL DIGLYCEN
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CONTROL OF CONTROL
BY SIMILARITY.
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CONTROL
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TA (IN REF. 2).
FB3FF1BD6 (PF. 2).
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P07811;
01-AUG-1988
01-AUG-1988
01-OCT-1996
PULLULANASE
                                                                  This SWI
between
                                                                                                                                                               *Katsuragi N., Takizawa N., Murooka Y.;

*Entire nucleotide sequence of the pullulan aerogenes W70.";

J. Bacteriol. 169:2301-2306(1987).

-I- CATALYTIC ACTIVITY: STARCH-DEBRANCHING
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Katsuragi N., Takizawa N., Murook
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                                                                                             (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PFORM MALTOTRIOSE.

I- SUBUNIT: HOMOTRIMER.

I- SUBCELLULAR LOCATION: ATTACHED TO THANCOM (PROBABLE).

I- SIMILARITY: BELONGS TO FAMILY 13 OF KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           AQGAGLPVSSK :
                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSRLDGLVVA
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(Rel. 08, Last sequence update)
(Rel. 34, Last annotation update)
PRECURSOR (EC 3.2.1.41) (ALPHA-
) (PULLULAN 6-GLUCANOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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.41) (ALPHA-DEXTRIN
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M16187;

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Best Local Sin
Matches 934;
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SIGNAL
CHAIN
LIPID
ACT_SITE
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ACT_SITE
SEQUENCE
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InterPro; IP
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                                                   TTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGS
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|TGSDKYGPYWVIPLTKESGSINVIVRDGTNKLIDSG-RVSFSDFTDRTVSVIAGNSAVY
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NPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLRDSVRGGGFFDSGDALRQNQG
                                                                                                                                                                                                                                         KLTPTTVSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILI----SATQ
                         NPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLRDAVRGGGPFDSGDALRQNQG
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Similarity 84.5%;
34; Conservative
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IPR000461;
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N-ACYL DIGLYCERIDE.

BY SIMILARITY.

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BY SIMILARITY.
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Pred. No. 1.6e
9; Mismatches
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(C STRAIN-MSBB / DSM 3109;

(C STRAIN-MSBB / DSM M.L., Dodson R.J.,

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(C STRAIN-MSB / DSM M.L., Dodson R.J.,

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GLUCOSIDASE) (P
PULA OR TM1845.
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033840;
30-MAY-2000
30-MAY-2000
30-MAY-2000
                                                                         This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
STRAIN-MSB8 / DSM 3109;
MEDLINE-98115241; PubMed-9453151;
Bibel M., Brettl C., Gosslar U., Kriegshaeuser G., Liebl Bibel M., Brettl Signar of genes for amylolytic enzymes "Isolation and analysis of genes for amylolytic enzymes hyperthermophilic bacterium Thermotoga maritima.";
FEMS Microbiol. Lett. 158:9-15(1998).
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Bacteria; Thermotogales;
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                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO FAMILY 13 (
KNOWN AS THE ALPHA-AMYLASE FAMILY
                                                                                                                                                                                                                                                                                                       (1-6)-ALPHA-GLUCOSIDIC FORM MALTOTRIOSE.
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1. 39, Last sequence update,
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21. 39, Last annotation update)
ECURSOR (EC 3.2.1.41) (ALPHA-DEXTRIN EN
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AJ001087; CAA04522.1; AE001821; AAD36907.1; TM1845; -.

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--GQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEV
                                                         T-TRIKEFRIMIQAIKQDLGMNVIMDVVYNHTNAAGPIDRISVLDKIVPWYYQRLNEITG
                                                                                                                                                                                                                                                                                                                                                          CDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEG
                                                                                                                                                                                                                                                                                                                                                                                                          NMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQFFSRLCEVNSAVKSSEFAGY 525
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                                        YDGKLIKSFALDPEETINYAACHDNHTLWDKNYLAAKADKKKEWTEEELKNAQKLAGAIL
                                                                                                                            QGIGSGAGVLPNELASLSDDOVRIILADLTRLGMAGNLADEVM--IDKDGAAKKG--SEID
                                                                                                                                                            IDPTIILYGEPWGGWGAPIRF---GKSDVAGTHVAAFNDEFRDAIRG-------
                                                                                                                                                                                    LNPDIYFFGEGWDS-NQSDRFEIASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQN
                                                                                                                                                                                                                 YLNESGCGNVIASERPMMRKFIVDTVTYWVKEYHIDGFRFDQMGLIDKKTMLEVERALHK
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ALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGAWSWQGGSDLK 361 AYPLGATYDGAGTNFSLFSEIAEKVELCLIDED-GVESRIPL--DEVDG-YVWHAYLPNI

Query Match Best Local S Matches 197

h 6.3%; Similarity 22.8%; 97; Conservative 11

Score 352.5; Pred. No. 1.4e 13; Mismatches

.4e-1 DВ

Indels Length

259;

Gaps

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197;

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RESULT 4
GLGX_MYCTU STANDARD; PRT; 721 AA.
AC 010767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLYCOGEN OPERON PROTEIN GLGX HOMOLOG (EC 3.2.1.-).
GN GLGX OR RY1564C OR MTCY48.01.
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A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,

A Badcock K., Basham D., Brown D., Chilingworth T., Connor R.,

A Badcock K., Basham D., Brown D., Chilingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,

A Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the

"Deciphering the Biology of Family 13 OF GLYCOSYL HYDROLASES, ALSO

KNOWN AS THE ALPHA-AMYLASE FAMILY STRONG, TO E.COLI AND
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                 EMBL; Z74020; CAA98327.1; -. HSSP; P10342; 1BF2.
TubercuList; Rv1564c; -.
  Hydrolase; Glycosidase.
ACT_SITE 362 362
ACT_SITE 470 470
SEQUENCE 721 AA; 810
                                                                                          InterPro; IPR000461; -
Pfam; PF00128; alpha-amylase;
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  470 B
81081 MW;
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    CRC64;
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RESULT 5
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032611;
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
SEQUENCE FROM N.A. MEDLINE-97340931;
                                            Bacteria; CFB g
NCBI_TaxID=239;
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                                                                                                            PRECURSOR
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-I- FUNCTION: HAS A HIGH RATE OF HYDROLYSIS FOR GLYCOGEN. DOES NOT CLEAVE PULLULAN. HAS A PH OPTIMUM OF 6-7.

-I- CAPALYTIC ACTIVITY: HYDROLYSIS OF 1,6-ALPHA-D-GLUCOSIDIC BRANCH LINKAGES IN GLYCOGEN, AMYLOPECTIN AND THEIR BETA-LIMITS DEXTRINS.
-I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY. ISOAMYLASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"An Isoamylase with neutral pH optimum from cloning, characterization and expression of Mol. Gen. Genet. 254:469-478(1997).
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                                                                                             TREWKAMVKAF-HDAGIKVYIDVVYNHTGEGGPWSGTDGLSVYNLLSFRGLDNPAYYSLS
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--- NSCQHGCFNFDKNDSGNALNR--IVAELPPRPAAGGAGADLIAEPWAIGGNSYQVGG
                                              ERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLRD--SVRGG----
                                                                                                                                              NETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAW
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                       J. MOI. Biol. 281:885-897(1998).
-i- CATALYTIC ACTIVITY: HYDROLYSIS
-i- LINKAGES IN GLYCOGEN, AMYLOPECI
-i- INDUCTION: BY MALTOSE.
-i- SIMILARITY: BELONGS TO FAMILY J
                                                                                                                                                                                 Amemura A., Fujita M., Futai M.;
"Transcription of the isoamylase gene
amyloderamosa SB-15.";
J. Bacteriol. 171:4320-4325(1989).
                                                                                                                         MEDLINE-98387895; PubMed-9719642; Katsuya Y., Mezaki Y., Kubota M.,
                                                                                                                                                                                                                                                                                                           Chen J.H., Chen Z.Y., Chow T.Y., Chen J.C., Tan S.T., Hsu W.H.; "Nucleotide sequence and expression of the isoamylase gene from isoamylase-hyperproducing mutant, Pseudomonas amyloderamosa JD2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1019
                                                                                           resolution.";
                                                                                                            *Three-dimensional structure of Pseudomonas isoamylase
                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                         MEDLINE-89327147; PubMed-2753857;
                                                                                                                                                                                                                                                                    SEQUENCE OF 744-776 FROM N.A.
                                                                                                                                                                                                                                                                                                Blochim. Blophys. Acta 1087:309-315(1990).
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and nucleotide sequence of the isoamylase gene from Pseudomonas amyloderamosa SB-15.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amemura A., Chakraborty R., Fujita
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           KNOWN AS THE ALPHA-AMYLASE FAMILY. ISOAMYLASE SUBFAMILY
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263:9271-9275(1988).
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7, Last annotation
R (EC 3.2.1.68).
                         TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                     AMYLOPECTIN
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EMBL; X13378; CAA31754.1;
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18F2; 12-AU
19R000461; -
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                                                                         KVYMDVVYNHTAEGGTWTSSDPTTAT----IYSWRGLDNATYYELTSGNQYFYDNTGIG
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                       ANFNTYNTVAQNLIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYN
                                               SDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFF
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F -> C (IN REF. 1).
GAS -> AH (IN REF. 1).
L -> V (IN REF. 1).
GAYT -> AVH (IN REF. 1).
SGLDLFAEPWAIGGNSYQLGGFPQGWSEWNGLFRDS
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AFRKAHPA -> RSARHIP (IN
F738BF8040246169 CRC64
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Pred. No. 1
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RESULT 7
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HSSP; P10342; 1BF2
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                                                                                                                                                                                                 InterPro; IPR000461; -
Pfam; PF00128; alpha-amylase;
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01-AUG-1992 (Rel. 23, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
ISOAMYLASE PRECURSOR (EC 3.2.1.68).
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Gen. Microbiol. 135:37-45(1989).
- CATALYTIC ACTIVITY: HYDROLYSIS OF
LINKAGES IN GLYCOGEN, AMYLOPECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: BY MALTOSE. SIMILARITY: BELONGS TO
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GLIGX_ECOLI STANDARD: PRT; 657 AA. P15067; P76693; 01-APR-1990 (Rel. 14, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) GLIYCOGEN OPERON PROTEIN GLGX (EC 3.2.1.-). GLIGX OR GLYX.

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                                                                              SP
                                                                                                                                                                                                                                                                                                                                                GEGWDSNQSDRFEIASQINLK----GTGIGTFSDRLR----DSVRGGGPFDSG------
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                                                                                                                                                                                                            --DESGSSNLFQSSGRSPWNSINFIDVHDGMTLKDVYSCNGANNSQAWPYGPSDGGTSTN
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                                                                                                                               NRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKS
                                                                                                                                                          YSWDQGMSAGTGAAVDQRRAARTGMAFEMLSAGTPLMQGGDEYLRTLQCNNNAYNLDSSA
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Pred. No. 1.8e:
36; Mismatches
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Best Local S
Matches 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Analysis of the Escherichia coli glycogen gene cluster suggests that catabolic enzymes are encoded among the biosynthetic genes."; Gene 70:363-376(1988).

1- FUNCTION: THIS PROTEIN MAY BE PART OF A GLYCOGEN BIOSYNTHETIC/CATABOLIC OPERON BUT IS NOT REQUIRED FOR GLYCOGEN SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.
Riley M., Collado-vides J., Glasner J.D., Rode C.K., M
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A.,
Mau B., Shao Y.;
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                      Clycogen
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000419; AAC76456.1; -. PIR; JT0400: BVECCY
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Bacteria; Proteobacteria; gamma
Escherichia.
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EMBL; U18997; AAA58229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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 51β
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CAUTION: REF. 2 SCOUENCE DIFFERS FROM THAT SHOWN DUE TO A STOP CODON IN POSITION 507.
                                                                                                                                                                                                                 JT0400; BVECGX.
 KSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEG
                                                                                                                                                                                                                                                          187;
                                                     LALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADTQQPFSRLCEVNSAV
                                                                              NAAIAPKCVVVVDHYDWEDDAPP-----RTPWGSTIIYEAHVKGLTYLHPEIPVEIRGTY
                                                                                                                                         YGYRVHGPWQ----PAEGHRFNPAKLLIDPCARQIDGEFKDNPLLHAGHNEPDYR-----D
                                                                                                                                                                     -----SWQGGSDLKGAFYRYAMTYYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLN 405
                                                                                                                                                                                                 GAHYDGQGVNFTLFSAHAERVELCVFDANGQ----EHRYDLPGHSGDIWHGYLPDARPGLR
                                                                                                                                                                                                                                                                                                                                                                                   PF00128; alpha-amylase; 1.
gen blosynthesis; Hydrolase;
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                                                                                                                                                                                                                                                                       Similarity
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73576 MW;
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BY SIMILARITY.
Y -> YY (IN REF
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Pred. No. 8.1e
04; Mismatches
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AA9EFC1F67FD0420 CRC64;
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                                                                                                                                                                                                                                                                    302.5;
No. 8.1
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yhew G.F.
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RESULT 9
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                                                    STRAIN-RD / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

FleisChmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.I.

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.I.

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                              Haemophilus influenzae
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAEL
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269:496-512(1995)
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                             assembly of Haemophilus
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                                                                                                                                                   Clayton R.A., Kirkness E.F., Dougherty B.A., Merrick J.M.,
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SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS PROTEIN MAY BE PART OF A GLYCOGEN BIOSYNTHETIC/CATABOLIC OPERON BUT IS NOT REQUIRED FOR GLYCOGEN SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAMTVY----HPQSRKVEQYEVTDPYAHSLS----TNSEYSQ----VVDLNDSA-LKPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NMVQHLKTLSASGVTHVELLPV-FDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAG
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                                                                                                                                                                                                      GMAGNLADFVMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKA
                                                                                                                                                                                                                                                 SYFAEWNDRFRDDLCRFWLWKSGE------
                                                                                                                                                                                                                                                                                                                                LGRDTPDFNSSAQLFTDIKNEPSLQ-NIKLIAEPWD-----IGHYGYQVGNFP
                                                                                                                                                                                                                                                                                                                                                                         -----GYHPKAQILSAWERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTF-
                                                                                                                                                                                                                                                                                                                                                                                                                   YYWRNDQGRYINWTGCGNMLNLSSD
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                                                                              KHNETNGEENRDGRNENYSYNHGVEGSTESLS----EPQKSAVENNRTFAQSGLLMSLL
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333 333 BY SIMILARITY.
                                                                                                                                                                                                                                                                            ·SDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRL
;|| || ;
                                     -YDSGDWFNRVDYS-----LQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGE
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; 75290 MW;
                                                                                                                     -----MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDS-----
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Pred. No. 1.2e
81; Mismatches
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.2e-07;
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EMBL; D31856; BAA06656.1; -.
EMBL; D2985; BAA06260.1; -.
EMBL; D83026; BAA11683.1; -.
EMBL; D83026; CAB15959.1; -.
EMBL; 799124; CAB15959.1; -.
FIR; S32920; S32920.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshida K.-I., Sano H., Seki S., Oda M., Fujimu "Cloning and sequencing of a 29 kb region of th genome containing the hut and wapa loci."; Microbiology 141:337-343(1995).
-!- FUNCTION: STILL UNKNOWN, NOT INVOLVED IN CEMOTILITY, SECRETION OR DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
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Bacteria; Firmicutes;
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01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
WALL-ASSOCIATED PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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NCBI_TaxID=1423;
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OR 32 (POTENTIAL).

WALL-ASSOCIATED PROTEIN.

3 X 101 AA APPROXIMATE TANDEM REPEATS.

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                                          LTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYLALTAGDSNMVQHLKTLSA
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31 X 21 AA APPROXIMATE TANDEM REPEATS OF X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
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RESULT 11
YF62_MYCTU STANDARD; PRT; 580
ID YF62_MYCTU STANDARD; PRT; 580
AC Q10769;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence upda
DT 30-MAY-2000 (Rel. 39, Last annotation up
DE HYPOTHETICAL 64.1 KDA PROTEIN RY1562C.
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MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
                                                                                                                               Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; My
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Hypothetical protein; Hydrolase; Glycosidase.
SEQUENCE 580 AA; 64076 MW; 506190468F44B862 CRC64;
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Rutter S., Seeger K., Skelton S., Squares S., Sqares R.
Raylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis
complete genome sequence.";
Nature 393:537-544(1998).
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Hornsby
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InterPro; IPR000461;
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                                                                       Query Match
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                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
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01-APR-1993 (Rel. 25, Last
01-OCT-1996 (Rel. 34, Last
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"The glgB gene from the thermophile thermolabile branching enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-93208370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus caldolyticus.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus
NCBI_TaxID=1394;
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SWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPD 412
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                                                                                                                                                                                               PF00128; alpha-amylase; 1.
                                                                                  Similarity
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309 309 BY SIMILARITY.
352 BY SIMILARITY.
420 420 BY SIMILARITY.
420 420 BY SIMILARITY.
1666 AA; 78096 MW; 1F64C31495BB1B6E CRC64;
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STRAIN-13.787

MEDLINE-98295987; PubMed-9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia

Badcock K., Basham D., Brown D., Chillingworth T., Connor

Badcock K., Basham D., Brown D., Chillingworth T., Connor

Badcock K., Basham D., Feltwell T., Gentles S., Hamlin N.,
                                                                                                                                                                                    O10625;
O1-OCT-1996 (Rel. 34, Created)
O1-OCT-1996 (Rel. 34, Last sequence update)'
O1-OCT-2090 (Rel. 40, Last annotation update)
PROBABLE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EGERANCHING ENZYME).
GLGB OR RV1326C OR MTCY130.11C.
                                                                                                                                           Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; My
                                                                                     STRAIN-H37RV;
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=1773;
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Glycogen blosynthesis; Transferase: Glycosyltransferase.
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-1- SUBUNIT: MONOMER (BY SIMILARITY),
-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL
 386
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                                                                         QDLGMNVIMDVVYNH----TNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSA
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                          PEHRMFAKLIADSLAVWTTDYKIDGFRFDL - - - MGYHPKAQILSAWERIKALNPDIYFFG
                                                         Q-AGIGVIVDWVPAHFPKDAWALGRFDGTPLYEHSDPKRGEQLDWGTYVFDF-----GR
                                                                                                                                               QSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAIK
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 InterPro: lenvource,
Pfam; PF00128; alpha-amylase; 1.
Clycogen blosynthesis; Transferase; Glycosyltransferase.
ACT_SITE 405 405 BY SIMILARITY.
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                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                               -i- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS
-i- SUBUNIT: MONOMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=RD / KW20 / ATCC 51907;
MEDLINE~95350630; PubMed~7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
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                                                                                                                                                        entities requires a license agreement (See or send an email to license@isb-sib.ch).
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RESULT 15

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STANDARD; PRT; 1861 AA.

AC P38536;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE AMYLOPULLULANASE PRECURSOR (ALPHA-AMYLASE/PULLULANASE) (PULLULANASE TYPE II) [INCLUDES: ALPHA-AMYLASE (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN DE GLUCANOHYDROLASE); PULLULANASE (EC 3.2.1.41) (1,4-ALPHA-D-GLUCAN DE GLUCANOHYDROLASE); PULLULANASE (EC 3.2.1.41) (1,4-ALPHA-D-GLUCAN DE GLUCANOHYDROLASE) (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
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                                                                                                                                                                                                                                                                                        YQ----
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Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPNQYGGRENLEAIEFLKHTNWKIHSEMAGAISIA
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Best Local S
Matches 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attachment to the cell surface.";

J. Bacteriol. 176:3295-3302(1994).

-:- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-!- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matuschek M., Burchhardt G., Sahm K., Bahl H.;
"Pullulanase of Thermoanserobacterium thermosulfurigenes EM1
(Clostridium thermosulfurogenes): molecular analysis of the g-
composite structure of the enzyme, and a common model for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-DSM 3896 / EMI;
MEDLINE-94252998; PubMed-8195085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoanaerobacter thermosulfurogenes (Clostridiu thermosulfurogenes).
Bacterla; FirmLoutes; Bacillus/Clostridium group; Thermoanaerobacter group; Thermoanaerobacterium.
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000461; -.
InterPro; IPR0011119; -.
InterPro; IPR001777; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                       NIAMOC
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Glycosidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00395; SLH; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M57692; AAB00841.1; -.
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                            933
                                                                                 882
                                                      61
                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: GLYCOSYLATED.

SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, KNOWN AS THE ALPHA-AMYLASE FAMILY.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS S-LAYER ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORM MALTOTRIOSE.
SGSDKYGPYWVIPLNKESGCINVIVR
                           PSNVVVTSGNGKVDLSWLQSDGATGY - - - NIYRSSVEGGLYEKIASNVTETTFEDANVTN
                                                                              KFLRDGVTFKDLI-----NNNVSYSISNGQIVIDVPAMSGVML----ISDDGQDLTAPQA
                                                                                                        RYTRNALVLGSLVLLSGCDNGSSSSSSSSGN--PDTPDNQDVVVRLPDVAVPGEAVTAVEN
                                                   QAVIHL-----VDIAGITSSSAADYSSKNLYLWNNE--TCDALSAPVAD--WNDVSTTP 110
                                                                                                                                        216;
                                                                                                                                                                                                                                                                                                                                                                                                                PF00128; alpha-amylase; PF00041; fn3; 2.
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POTENTIAL.
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
SLH 1.
SLH 2.
SLH 3.
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Pred. No. 0.38;
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BY SIMILARITY.
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06C23070E453B574 CRC64;
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 PNDSITR-EEMTAIAMRA
                                                                                                                                            SSGTITFNATHFSQYAAFEYDKTFNDIKDNWAKDVIEVLASRHIVEGMTDTQYEPNKTVT
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                                                                                                                                                                                                                                                                                                                         SVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDD-----QVRHLADLTRLGMA
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                                 -YEVITRVKEMVATPGEAELKOMTAFYQELTELRKSS
                                                                        RAEFTAMILRILNIKDETYSGEFSDVKSGDWYANAIEAA - - - -
                                                                                                              RDSY - - -
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YEMLTOYKEEN
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sp_bacteria:*
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Q41386 spinacia o1
O81638 zea mays (m
O48541 hordeum vul
Q9rxb0 delinococcus
O64454 oryza sativ
P93416 oryza sativ
P71095 bacteroides
O9xdb5 fervidobact
P7098 bacteroides
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ALIGNMENTS

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RESULT
Q9KZ11
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STRAIN-A3(2);
A Redenbach M., Kleser H.M., Denapalte ...
A Redenbach M., Kleser H.M., Denapalte ...
A Kinashi H., Hopwood D.A.;
A Kinashi H., Hopwood D.A.;
The 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RI Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL355752; CAB90874.1;
CROUENCE 1798 AA; 194106 MW; 43D13868FACF5C6A CRC6/
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STRAIN-A3(2);
Seeger K.J., Harris D.
Submitted (MAY-2000) 1
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE BIFUNCTIONAL PROTEIN (SECRETED ALPHA-AMYLASE/DEXTRINASE).
SC10B7.21C.
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STRAIN-A3(2);
Cerdeno A.M., Parkhill J., F
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Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Streptomyces.
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DKDGNKDVAADRTIDVTETGEVWIEQGEEQLVTERPEYPAQDTTKAVLHYKRADGNYDGW 852
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e EMBL/GenBank/DDBJ databases.
                                                                                                                  Score 1667.5;
Pred. No. 4.4e:
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TVPARTVAVFQ
                               TLPAWSVAVLE
                                                              -----RLGDLVVVFNATPERQEQRVGAAAGTGYRLHPVQAAGADAVVKESAYAAKTGTF
                                                                                           GASLDSRLDGLVVAINAAPE--SRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADGTV 1064
                                                                                                                             CPQITGASAAYRDLLRIRSGEQDFSLATAARVQSRLSFPLSGEDETPGVITM-----
                                                                                                                                            EAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKA 1006
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Submitted (JAN-1995) to the EMBL/GenBank/DDBJ
EMBL, X83969; CAX58003.1; -.
MENDEL; 16403; Spiol;2480;16403.
INTERPRO; IPR000461; -.
PFAM; PF00128; alpha-amylase; 1.
CHAIN 65 964
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-8 WEEKS OLD LEAVES;
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                                                                                 QRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQIL
                                                                                                                                                                                             GSYATDPEGTTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYY
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                                                        LR-RDNDGAIENSTCVNDTASEHFMVERLILDDLKHWAVNYKVDGFRFDLMGHIMKHTMV
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                                                                                                                                                                                                                                                                         -KKWKF------VDTKRFETLPPDSEEQQAQITAIRDEDGYNWGYNPVLWGTPK
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-IYFFGEGWDSNQ---SDRFEIASQINLKGTGIGTFSDRLR
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Matches
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
EMBL; AF080567; AAD11599.1; -
MENDEL; 32273; Zeama; 2480; 32273.
SEQUENCE 962 AA; 106239 MW; 5F5AAB7C6EBD5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (Trembirel. 08, Created)
01-NOV-1998 (Trembirel. 08, Last sequence update)
01-NOV-1999 (Trembirel. 12, Last annotation update)
PULLULANASE-TYPE STARCH DEBRANCHING ENZYME.
                                                                                                                                                                                                                                                                                                                                                 Beatty M.K., Rahman A., Myers A.M., James M.G.; "Genetic and biochemical characterization of ZPU1, a pullulanase-type
                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays (Maize).
Eukaryota; Viridiplantae;
Magnoliophyta; Liliopsida;
MCBI_TaxID=4577;
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                                                                                                                                                           GVAVAESAQGFLLDARAYWVTKSLIAWNISDQKTSLFLYASRNATMCMSSQDMKGYDSKV
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QLNELNGVWSVTGPRNWENRYYLYEVTVYHQTTGNIEKCLAADPYARGLSANSTRTWLVD
                                                  LPGVLDDMFAYTG----PLGTIFSEEAVSMYLWAPTAQDVSVSFYDGP-----AGPLLETV
                                                                                                       ELQPENDGLPSSVTQKFPFISSYRAFRIPSSVDVATLVKCQLAVASFDAHGNRQDVTGLQ
                                                                                                                                KLTPTT--VSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQ
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                       --DSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta; ; Poales; Poaceae; Zea.
                                                                                                                                                                                                                Score 1432.5; DB
Pred. No. 1.4e-82;
73; Mismatches 338
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048541;
01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-MAY-2000 (TrEMBLrel. 1
LIMIT DEXTRINASE.
           STRAIN-CV. IGRI;
Lok F. Kristensen M., Planchot V., Leah R., S
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ
EMBL; AF022725; AAD04189.1; -
MENDEL; 27102; Horvu; 2480; 27102.
INTERPRO; IPR000461; -
IPFAM; PF00128; alpha-maylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1039
                                                                                                                                                                                                                                  Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
Magnoliophyta; Liliopsida;
    SEQUENCE
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                                                                                                               SAYEAATGRFTVPGRTVSVFVEPR
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MEDILINE-99169277; PubMed-10069825;
Burton R.A., Zhang X.Q., Hrmova M., Fincher G.B.;

"A single limit dextrinase gene is expressed both endosperm and in germinated grains of barley.";
Plant Physiol. 119:859-872(1999).

EMBL; AF122050; AAD34348.1; -.

EMBL; AF122049; AAD34347.1; -.
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Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
MCBI_TaxID=4513;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAY-2000 (TrEMBLrel. 13, Last annotation
LIMIT DEXTRINASE.
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                                                                                                        TVPAELRGKYLALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPF
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IQIGLAGNLRDYVLISHTGEAKKGSEIHTFDGLPVGYTASPIETINYVSAHDNETLFDVI
                                                                                 GIGSFNDRIRDAINGGNPF--GNPLQ--QGFNTGLFLEPNGFYQGNEADTRRSLATYADQ
                                                                                                                                                                                                                                                                                                       VLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDL
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                                        TRLGMAGNLADFVMIDKDGAAKKGSEI-DYNGAPGGYAADPTEVVNYVSKHDNQTLWDMI 850
                                                                                                                                                                          MGH I MKRTMMRAKSALQSLTTDAHGVDGSK I YLYGEGWDFAEVARNQRG I NGSQLNMSGT
                                                                                                                                                                                                                 MGYHPKAQILSAWERIKALNPD-----IYFFGEGWDSNQ---SDRFEIASQINLKGT
                                                                                                                                                                                                                                                              VLDKIVPGYYVR-RDTNGQIENSAAMNNTASEHFMVDRLIVDDLLNWAVNYKVDGFRFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRLCEVNSAVKSS-EFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVDSDSRGAFRAFAYQASAGMEHLRKLSDAGLTHVHLLPSFHFAGVDD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVVASFGADGKHVDVTGLQLPGVLDDMFAYTG---PLGAVFSEDSVSLHLWAPTAQGVSV
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9RXB0
                                                                                                                                                                                                                                                                                                      radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001900; AAF09983.1;
TIGR; DR0405; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                   AEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGAWSWQG
                                                                                                                                       AIMLSRDLIVVKPALAQPGAW----LTLHVSPTATLKLGADGVSGGDTLALEEVEGGLTP
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 DQSWKGLAYRFEVRVFAPSTGNIETNLVTDPYSVALTRNSTHSVFADLSDNSQKPAGWNA
                       GSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDN
                                               AYAG---PLGVTWQGNKPTVRLWAPTAQDVKLHVSRPDGTQERTLPMTRDT-QGVWTASG
                                                                                            ALQAKAPYLAGYKLLQIRAADRAKLPTALSGQLAVSSVLPGGKVLDATGVQTAWALDDLY
                                                                                                                QVSMRFPHLSSYAAFKL--PDNANVDELLQGETVAIAAAEDGILISATQVQTAGVLDDAY
                                                                                                                                                        -VALAEAHWVDKNTLLWPGGQDKPTVRLYYSHSS--KVAADGEGKFTDRYLKLTPTTVSQ
                                                                                                                                                                                     LGFIVHKGDDKDPGPD-----GTLTREQGNQLWIVSGNPTPSTTRPDTRVRTVGDLKQQQ
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larity 35.3%;
Conservative 15
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                                                                                                                                                                                                                                                                                            97926 MW;
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Pred. No. 6.4e
57; Mismatches
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                     Oryza sativa (Rice).
Eukaryota; Viridiplantae; |
Magnoliophyta; Liliopsida;
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 SEQUENCE
                                                                            STRAIN=CV. NORIN-8;
Francisco P.B., Zhang
             PFAM; PF00128;
                                                                     Nakamura Y.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID-4530;
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alpha-amylase;
AA; 109858 MW;
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                                  Submitted (APR-1998) to the EMBL/GenBank/DDBJ
EMBL; AB012915; BAA28632.1;
MENDEL; 28470; Orysa;24480;28470.
INTERPRO; IPR000461;
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                                                                                                                                                                                                                                        Embryophyta; Tracl
; Poales; Poaceae;
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9D537693EF154A4E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              HFASVDDNKSNWKFVD-----EAQLAKLPPGSDEQ
KCRETVPRRTTAVEVQPR 987
                                                                                                                                                                                                          LRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAE
                                                                                                                                                                                                                                                       SPVETINYVSAHDNETLFDIVSIKTPIGLSIDEKCRINHLASSMIALSQGIPFFHAGDEI
                                                                                                                                                                                                                                                                             DPTEVVNYVSKHDNQTLMDMISYKASQEADLATRVRMQAVSLATVMLGQGIAFDQQGSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLATV--NEFSDKVADIQQPESRLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQ-SDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVHLHFRLFRLNLLNDFCSPPITKHPGRIMETVMQDSAGIRHLRKLSAAGLTHVHLLPSF
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                               DGTVTLPAWSVAVLELPQ
                                                               EKCKMAQLDKNFSYVVTIFNVCPHEVSIEIHDLASLGLELHPIQVNSSDALVRQSAYEAS
                                                                                           AG---ASLDSRLDGLVVAINAAPE--SRTLNEFAGETLQLSAIQQTAGENSLANGVQIAA 1060
                                                                                                                           LKQ--MTAF--YQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMK 1005
                                                                                                                                                                                                                                                                                                                      NGYYQGNEADTRRELATYADHIQIGLAGNLKDYVLRTHTGEAKKGSDIYTFDGSPVGYTS
                                                                                                                                                                                                                                                                                                                                       NELASLSDDQVRH----LADLTRLGMAGNLADFVMIDKDGAAKKGSEI-DYNGAPGGYAA 829
                                                                                                                                                                                                                                                                                                                                                                                  FGEVAQNKRGINASQINMSGTGIGSFNDRIRDSVNGGNPF--GNPLQ--QGFSTGLFLEP
                                                                                                                                                                                                                                                                                                                                                                                                   RVVMDVVYNHLDSSGPFGVSSVLDKIVPGYYLRRN-VNGQIENSAAMNNTASEHFMVDRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAIKQDLGM 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPLLQTVQLKELNGVWSVTVPRYPENQYYLYEVKVYHPSTSQVEKCLADDPYARGLSANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDVTGLQLPGVLDDMFAYTG----PLGAVFSDKDVDLYLWAPTAQDVRVCFYDGP-----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFTDRYLKLTP--TTVSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGIL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRDGVGEECAAAVASQGFVTDARAYWVTRSLIAWNVNDQDTSLFLYASRDATMHVSDGAI 123
                                                                                                                                                                                           LRSKSLDRDSYNSGDWFNKLDFTYETNNWGVGLPPRDKNEENWHLI----KPRLENPSFRP
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P93416;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
STARCH DEBRANCHING ENZYME PRECURSOR.

Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

MCBI_TaxID=4530;
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MEDLINB-96275956; PubMed-8680309;
Nakamura Y., Umemoto T., Ogata N., Kuboki Y., Yano M., Sasaki T.;
Nakamura Y., Umemoto T., Ogata N., Kuboki Y., Yano M., Sasaki T.;
"Starch debranching enzyme (R-enzyme or pullulanase) from developing
rice endosperm: purification, cDNA and chromosomal localization of the
gene.";
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EMBL; D50602; BAA09167.1; -. 02.
MENDEL; 16402; Orysa;2480;16402.
INTERPRO; IPR000461; -.
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                                                                                                                                                                                                   DNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAIKQDLGM
                                                                                                                                                                                                                                                                                                                                 KFTDRYLKLTP--TTVSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGIL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRDGVGEECAAAVASQGFVTDARAYWVTRSLIAWNVNDQDTSLFLYASRDATMHVSDGAI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNSAVYDSRADAFRAAFGVALAEAHWVDKNTLLWPGGQDKPIVRLYYSHSSKV-AADGEG
                                                                                        NVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKL
                                                                                                                                                                           ----QAAIVSIQQEDPYNWGYDPVLWGVPKGSYASNPDGPSRIIEYRQMVQALNR-IGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLAL-----TAGDSNMYQHLKTLSASGVTHVELLPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDVTGLQLPGVLDDMFAYTG---PLGAVFSDKDVDLYLWAPTAQDVRVCFYDGP----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISATQVQTAGVLDDAYABAABALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGYDSKIELEPEHASLPDNVAEKFPFIRSYRTFRVPSSVDVASLVKCQLAVASYDAHGRH
                                                                                                                                                                                                                                                                                                  HFASVDDNKSNWKFVD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYSQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGK 456
IADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPD----
                                                       RVVMDVVYNHLDSSGPFGVSSVLDKIVPGYYLRRN-VNGQIENSAAMNNTASEHFMVDRL
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109592 MW; FBAB89E1634CAD27 CRC64;
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                                                                                                                                                                                                                                                                                            EAGLAKLPPGSDEO
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Present J.N., Salyers A.A.;

"Contribution of a neopullulanase, a puglucosidase to growth of Bacteroides the J. Bacteriol. 178:7173-7179(1996).

EMBL; U67061; AAC44685.1;

INTERRO; IPRO00461;

PFAM; PF00128; alpha-amylase; 1.

SEQUENCE 668 AA; 74603 MW; 044D3D6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (
01-FEB-1997 (
01-MAY-2000 (
PULLULANASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-5482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; CFB 9
NCBI_TaxID-818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteroides thetaiotaomicron.
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                                                                                                                                                                                                                                                                                                                  Local Similarity
les 215; Conserv
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                                                                                                                                                                                                                                                              VQTAGVLDDAYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHP---
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  AAIIDWQST - - NPDGWESDTRP - PLKSPAD-
                                                                                                                                                                                                             VRTGSLIEMEYTPEA-----
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                                              SQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYL 458
                                                                                                     VKMQSGEEGTWTAVVSKDLIGKFYTFNV-----KIDDKWQGDTPGINARAVGVNGKR
                                                                                                                                                      -MTRDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVE---QYEVTDPYAHSLSTNSEY
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                                                                                                                                                                                                                                                                                                            %; Score 722; DB 2;
%; Pred. No. 1.1e-37;
117; Mismatches 231
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Last annotation update)
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044D3D62578C6845 CRC64;
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---MIIYEMHHRDFSV-DSTSGVKNKGKYL
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Q9XDB5;
Q1-NOV-1999
Q1-NOV-1999
Q1-MAY-2000
MEDINE-DS. AUGUST PUBMED-10224005;
MEDINE-DS. AUGUST P. Jorgensen P.L., Antranikian G. Pertoldo C., Duffner F., Jorgensen P.L., Antranikian G. Pullulanase type I from fervidobacterium pennavorans v sequencing, and expression of the gene and biochemical characterization of the recombinant enzyme. Appl. Environ. Microbiol. 65:2084-2091(1999).
EMBL, AF095662; AAD30387.1; -.
INTERPRO; IPRO0408; -.
INTERPRO; IPRO0408; -.
PROSITE; PS00626; RCC1_2; UNKNOWN_1.
SEQUENCE 849 AA; 96591 MW; 1CB6BZA88ZA351A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fervidobacterium pennivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PULLULANASE
                                                                                                                                                                                                                                                                                                  STRAIN-DSM 9078
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Query Match Best Local Similarity

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Matches

243;

Conservative

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Score 716; DB 2; Pred. No. 4.1e-37; 39; Mismatches 315

Length 849;

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Best Local Similarity
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Hatada Y., Igarashi K., Ozaki K., Ara K., Hitomi J., Kobayashi T.,
Kawai S., Watabe T., Ito S.;
"Amino acid sequence and molecular structure of an alkaline
amylopullulanase from Bacillus that hydrolyzes alpha-1,4 and alpha-1,6
linkages in polysaccharides at different active sites.";
J. Biol. Chem. 271:24075-24083(1996).
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
ALKALINE AMYLOPULLULANASE.
Bacillus sp.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID-1409;
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INTERPRO; IPR000834; -.
INTERPRO; IPR001894; -.
INTERPRO; IPR001894; -.
PFAM; PF00128; alpha-amylase; 2.
PFAM; PF00726; Gram_pos_anchor; 1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
SEQUENCE 1938 AA; 214917 MW; A29D3F715EB6A72E
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                                                                                                                                                                              AELRGKYLALTAGDSNMYQHLKTLSASGYTHVELLPVFDLATVNEFSDKVADIQQPFSRL 510
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                                                            CEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPF 570
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                                                                                                                                EDLKAQFGTF----ASFVEKLDYIQELGVTHIQLLPVMSYYFSNEF-----ESGERM
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24.2%; Pred. No. 5.1e-35;
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01-NOV-1996 (Tremblrel. 01, Last sequence update)
01-MAY-2000 (Tremblrel. 13, Last annotation update)
ALPHA-DEXTRIN 6-GLUCANOHYDROLASE (EC 3.2.1.41)
(ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE) (PULLULANASE)
(PULLULAN 6-GLUCANOHYDROLASE) (LIMIT DEXTRINASE) (DEBRANCHING ENZYME)
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Q59319;
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                                                         Hydrolase;
SEQUENCE
                                                                                EMBL; L39876; AAB06264.1;
INTERPRO; IPRO00461;
PFAM; PF00128; alpha-amylase;
                                                                                                                                           Albertson G.D., McHale R., Gil
Eur. J. Biochem. 0:00(0).
-i- CATALYTIC ACTIVITY: STARCH
ALPHA-GLUCOSIDIC LINKAGES
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825 AA; 95
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AND STARCH
             Length
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Lapidus A.
Submitted ([2]
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O1-JAN-1998 (TrEMBLrel.
O1-JAN-1998 (TrEMBLrel.
O1-MAY-2000 (TrEMBLrel.
                                                                  Bacillus subtilis.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID-1423;
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                  SEQUENCE FROM N.A.
Lapidus A., Galleron
Submitted (JUN-1997)
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                                                                                                                                       PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                     MPRISDDGSNYEVITRYKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKR 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQE----ADLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTVKQSRQVANEVRKRNPKALVYGEGWVMGNSTCLVEEMATILSSCHQGYSIGLFNDRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPKAQILSAWERIKALNPDIYFFGEGWDSNQSDRF--EIASQINL--KGTGIGTFSDRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVPEYFYRVDD-YGDYSNATGCGNELATEKPMVRKFILDTIIYWTEEFHIDGFRFDLMGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AENGTWDVYLPGDLKNHFYLYEIWHYNYEDDEGYIVYHVPDPYSKASSSNSGKSYIFDPA
                                                                                                                                                                                                                                                                                                                                                                                                           TRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAIRG-----DLDGYKTGY----
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                                                                                                                                                                                                                                                                                                                                                                                  -LANAIVLTSQGVAFLHGGVEFNRSKGGHPNTYNAGDNINKIDWSLKEKFFDT+
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                  Sorokin A., Ehrlich I
he EMBL/GenBank/DDBJ
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Last annotation updat
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                                Ehrlich D.
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Coldwell B., Capuano V., Carter N.M.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chol S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chol S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chol S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chol S.K., College P., Goffeau A., Gollghtly E.J., Grandi G.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gulseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Gulseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Ricger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Schiguchi M., Tamakoshi A., Tanaka T., Takahashi H., Takamaru K.,
RA Viari A., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler E., Wedler E., Westzenegger T.,
RA Viaria K., Waller E., Wedler E., Wedler H., Weitzenegger T.,
RA Viaria K., Walmoto K., Vatan K.,
RA Viaria K., Vatan K., Serror S., Vasumoto K
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Best Local Similarity
Matches 224; Conserv
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                                                 569
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                          PFHYTVPEGSYATDP-EGTTRIKEFRTMIQAIKQDLGMNVIMDVVVNHTNAAGPTDRTSV 627
                                                                                                                                                                               KYLALTETDTQTANGSSSGLAYVKEL---GVTHVELLPVNDFAGVDE-----EKPL-
                                                                                                                                                                                                         KYLALTA-----GDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQTAGVLDDAYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHP--- 342
PLHFFAPEGSYASNPHDPOTRKTELKOMINTLHOH-GLRVILDVVFNHVYKR----ENSP
                                                                                                                                RLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYD 568
                                                                                                                                                                                                                                                                                                        YSQVVDLNDSALKPD--GWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRG 455
                                                                                                                                                                                                                                                                                                                                                                 GRTFQMTR-LEKGYYAYTYTGDLHG--YEYLFCI----CNNSEWMETYDQYAKAYTYNGE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRTAAFDDEFYYDG----ELGAVYTADHTVFKVWAPAATSAAVKL-----SHPNKS
                                                                                                                                                                                                                                                                            KGVV-----LRPDQMKWTAPLKPFSHPVDA----VIYETHLRDFSIHENSGMIN-KG
                                                                                                                                                                                                                                                                                                                                                                                                              -----MTRDSASGAWSWOGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSE 397
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AA; 81104 MW; 96F9EB7667877E93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 647.5; DB 2; 27.1%; Pred. No. 6.9e-33; tive 99; Mismatches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 718;
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324 126	270 VAIAAAEDGILISATQVQTAGVLDDAYAEAAEALSYGAQLADGGVTFRVWAPTAQ 3 :	pb dy
269 73	210 YSH8SKVAADGEGKFTDRYLKLTPTTVSQQVSMRFPHLSSYAAFKLPDNANVDELLQGET 2	gb 99
209 47	150 AFGDETDRTVSVIAGNSAVYDSRADAFRAAFGVALAEAHWVDKNTLLWPGGQDKPIVRLY 2	D 03
, ps 35;	Ouery Match 11.2%; Score 630; DB 2; Length 718; Best Local Similarity 27.1%; Pred. No. 9e-32; Matches 232; Conservative 92; Mismatches 282; Indels 250; Gap	¥ 8 0
	PFAM; PF00128; alpha-amylase; 1. SEQUENCE 718 AA; 80446 MW; 8F7C0D22405EA8A8 CRC64;	DR
	mitted (APR-1998) to the L; aF060205; AAC15073.1; ERPRO; IPR000461;	DR RIL
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	Bacteria; Thermus/Deinococcus group; Thermus group; Thermus. NCBI_TaxID=275; [1]	# 0 0 0
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	01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	D
	009008 PRELIMINARY; PRT; 718 AA. 069008;	
	UULT 14	RESU
	672 LPNDIPYRLLCDPSGFQEDPTEIKKTVAVNGIGTVIL 708	Ф
	FAGETLQLSAIQQTAGENSLANGVQIAAD	Qy
671	622RSAADIQRHLECLTLKEHLIAYRLYDLDEVDEWKDIIVIHHASPDSVEWR	Ф
1027	AGASLDSRLDGLVVAINAAPES	γ
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977	KSSPLFTLGDGSA	Qy
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540	KALAPIVPRPSQSINYVESHDNHTFWDKMSFALPQE KALAPIVPRPSQSINYVESHDNHTFWDKMSFALPQE	Db 5
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799	SDDQVRHLADLTRLGMAGN	P 04
468	ATPLPHEQKAALANAPRMPGIGFFNDMFR	Db
745	KGTGIGTFSDRLR	Qy
408		DЬ
687	KIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLM	Qy

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RESULT 15

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ID Q9K6N1
AC Q9K6N1
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DE ALKALI
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                                                    SEQUENCE FROM N.A.
STRAIR-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001519; BAB07416.1; -.
SEQUENCE 1072 AA; 120674 MW; 5264235CF24619D9 CRC64;
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                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                        Bacillus/Staphylococcus
NCBI_TaxID=86665;
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 Local Similarity
                Match
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                                                                                                                                                                                                                                                                                                                                                                      AFRLATEAEVLRHFTF
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                              YEV--ITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLG---DGSAVMKRVD--- 983
                                                                                                                                                         TLWDMISYKASQ-----EADLATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKS-----
                                                                                                                                                                                                               LADLTRLGMAGNLADFVMIDKDGAAKKGSEI--DYNGAPGGY-AADPTEVVNYVSKHDNQ 844
                                                                                                                                                                                                                                                                              QINLKGT-GIGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRH
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                                                                                                                                                                                                                                                                                                                       GLDPYAKSMAAWNNEGSYSI-----GKAAIVDPSSIGPELDFAEIEGFEKREDAI 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAENIGFLVL-----NTATGDKDGND-KHVQLLSPEM----KEIWIKEGSDDVFL 140
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                                                                                                                                                                                                                                                                                                                                                                                    YNHTAA-----VEIFEDLMPNYYHFM-DADGTPRTSFGGGRLGTTHKMSRRILVDSITY 660
                                                                                                                                                                                                                                                                                                                                                                                                                   YNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAV 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTLVAQTDSYNWGYDPFHYTVPEGSYATDPEG-TTRIKEFRTMIQAIKQDIGMNVIMDVV 612
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YPIHHLTR---
                                                               GGQAPYKSTYMTDENGKPFVYPYFIHDSYDSSDAINKFDWGKATNK------EK 898
                                                                                                                               TLHDVIAQSIRKDPEYHQEEIHKRIRL---GNTMVLTAQGTAFLHAGQEFGRTKQFRADT
                                                                                                                                                                                                                                                          QDWMQHTESVGVFSDEFRNELK------SGFG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---VIGSHPMTRDSASGAWSW------QGGSDLKGAFYRYAMTVYHPQSRKVEQYEVT-- 385
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                                                                                             -FTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSN
TYTAGLIELRRSTNAFTHGTLVDVQANVRLLDIPE
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